

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:49 : Search time 22 Seconds
(without alignments)
1712.941 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFEDLPEDPRSPRPAK.....KAVQSGADNVYVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481	23.8	341	2	G86315 hypothetical prote
2	474	23.5	242	2	T18588 probable protein p
3	401.5	19.9	300	2	A55804 phosphoprotein pho
4	370.5	18.4	414	2	S62462 protein phosphatas
5	368	18.2	389	2	T05095 hypothetical prote
6	368	18.2	975	2	T08606 protein phosphatas
7	365	18.1	359	2	T52337 phosphoprotein pho
8	364.5	18.1	348	2	T50783 protein phosphatas
9	362	17.9	464	2	H66700 protein F12A21.5 l
10	358.5	17.8	361	2	T45778 protein phosphatas
11	353.5	17.5	355	2	H84643 probable protein p
12	352.5	17.5	434	2	T04263 phosphoprotein pho
13	352	17.4	392	2	F84650 hypothetical prote
14	351	17.4	404	2	T00750 probable protein p
15	350	17.3	357	2	T06308 protein phosphatas
16	348	17.2	370	2	S54257 protein phosphatas
17	347	17.2	348	2	E88434 protein F23F11.1 l
18	347	17.2	356	2	T25181 hypothetical prote
19	340	16.8	382	2	S22422 phosphoprotein pho
20	340	16.8	382	2	A32399 phosphoprotein pho
21	338.5	16.8	383	2	T48018 hypothetical prote
22	338.5	16.8	390	2	C84826 protein phosphatas
23	338.5	16.8	405	2	F86206 hypothetical prote
24	338	16.7	382	2	I53823 magnesium dependen
25	337.5	16.7	380	2	E84748 probable protein p
26	336.5	16.7	381	2	T09640 protein phosphatas
27	336.5	16.7	396	2	T02483 phosphoprotein pho
28	336	16.7	382	2	S22423 phosphoprotein pho
29	326	16.2	390	2	S65672 phosphoprotein pho

30	326	16.2	393	2	I49016 phosphoprotein pho
31	442	15.9	442	2	B86209 protein F2265.22 l
32	319	15.8	390	2	S20392 phosphoprotein pho
33	319	15.8	397	2	JC2524 phosphoprotein pho
34	317.5	15.7	281	2	S41854 phosphoprotein pho
35	309	15.3	468	2	T21331 hypothetical prote
36	307	15.2	816	2	T48123 hypothetical prote
37	306	15.2	347	2	A56058 phosphoprotein pho
38	305.5	15.1	464	2	S50592 hypothetical prote
39	305	15.1	388	2	C85323 protein phosphatas
40	302	15.0	386	2	T09019 phosphoprotein pho
41	300	14.9	491	2	T16354 hypothetical prote
42	297	14.7	423	2	T48121 hypothetical prote
43	292.5	14.5	511	2	F96752 protein phosphatas
44	289	14.3	468	2	S39832 probable protein p
45	284	14.1	362	2	F84695 probable protein p

ALIGNMENTS

RESULT 1

G86315

hypothetical protein T10F20.4 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C:Accession: G86315

R:Theoploids A.: Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Comp. L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Malt, R.; Marzla

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Selzberg, S.L.; Schwartz, J.R.; Shum, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.K.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G86315

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <STO>

A:Cross-references: GB:AE005172; NID:g9719738; PIDN:AAF7840.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

Query Match 23.8%; Score 481; DB 2; Length 341;
Best Local Similarity 35.8%; Pred. No. 9,1e-28;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;

OY	78	KRTSPSEKNGSEELV-----EKKVCASVI-----FGLKGYVAERKGEREMODAHYI	127
DB	24	KAKKSEVSGGGEAAVAGNREAEEDKPSFVSEKKEFLVEADVAEDKGARHTMEDVWV	83
OY	128	LNITPECHPSPSLITRYSFAVPDGGIGIRASKFAFQNLHONLIRKFPKGDVYSVEKTV	187
DB	84	LPASLDF--PGTL--KRAHFAIYDHGGGLAAEPKRIHLNIVSAGLPRELLDV-KVA	138
OY	188	KRCLLDTEKHNDEEFLKASSQKPAWKDGSTACVLAVDNITLITANLQDSALICR----	243
DB	139	KRAILTEGFKTDELQVSVS--GGWODGATACVWVILQKVFANLGDRAAVLANSTTT	196
OY	244	-----YNEESOKHAALSLSEKHNPTQYEEEMRIQKAGNV--RDGTVGLVEVSRIGDQO	297
DB	197	NELGNTEAGNPLKAIYITREHKAIVPEERSRQKSGGVISSNGLOGRLEVSATGDRH	256
OY	298	YKRCGYTSPVDIRRCOLTPNDRFTLLACDGLFKVFTPEEAVNFTLSCELEKTIOTREGKS	357
DB	257	FKKFGVSAPPDIDHAFELERENFMILCCDIMEVFSPDAVGFOKLT-----KEG--	307
OY	358	AADAREACNRLANKAV-QRGSADNVYVWV	388
DB	308	---LHVSTVSRRLVKEAVKERCKNDCTAIVI	336

```

RESULT 2
T18588
probable protein phosphatase - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18588; T21693
R:Mortimore, B.
submitted to the EMBL Data Library, December 1998
A:Reference number: 218993
A:Accession: T18588
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-242 <W1>
A:Cross-references: EMBL:AL031264; PIDN:CAA20326.1; GSPDB:GN00020; CESP:F33A8.6
A:Experimental source: clone VF45EL0L
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: 219459
A:Accession: T21693
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-242 <W12>
A:Cross-references: EMBL:Z81525; PIDN:CAB04260.1; GSPDB:GN00020; CESP:F33A8.6
A:Experimental source: clone F33A8
C:Genetics:
A:Gene: CESP:F33A8.6
A:Map position: 2
A:Introns: 28/1; 101/1; 133/2; 202/2

Query Match      23.5%; Score 474; DB 2; Length 242;
Best Local Similarity 40.2%; Pred. No. 1.9e-27;
Matches 98; Conservative 54; Mismatches 80; Indels 12; Gaps 5;

QY 82 SEEEKNGSEELV---EKKVCASSVITGLKGYAEKRGEEEMODAHVILN--DITEBC 135
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 3 SDSRRSSDDLLDNDSEKSKRPRESNLYCTLAAYGCRGERADMODTHIMLPKFLGTE- 61

QY 136 RPPSLIRVSYFAVFDGHHGIRASKFAAQNHLNLRKPR--GVVISVEKTKRCLDIT 194
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 62 ---KSLFRASFAITFDGHAGFRAEHCOQOMGKTVKEKLAFSFPPLTSLKOTFTES 118

QY 195 FKHNDDEFLKQASSQKPAKMDGSTATCYLAVDNILYIANLGDSPRAITLRYNEESQKHNL 254
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 119 YKAVDDGLALAKQKPKIMKDOTATATMILNNVIYVANIGDSRAVAVAKKKEG--SFAPV 177

QY 225 SLKSHNPTQYEERKIRKAGGNVNDGRLVLEYSRISIGDQYKRCGVTSVPDIRCOL 314
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 178 CLTYVDHDPMSHDERMIRKAGAVVKGDRINGVIEYSRISIGDLPFKSLGIISTPDLKLTLL 237

QY 315 TPND 318
   | | |
Db 238 TKND 241

RESULT 3
A55804
phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramedium tetraurelia
C:Species: Paramedium tetraurelia
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 07-Dec-1999
C:Accession: A55804
R:Klump, S.; Hanke, C.; Donella-Deana, A.; Beyer, A.; Kellner, R.; Pina, L.A.; Schultz, J. Biol. Chem. 269, 32774-32780, 1994
A:Title: A membrane-bound protein phosphatase type 2C from Paramedium tetraurelia. Purified
A:Reference number: A55804; MUID:95105156; PMID:7806499
A:Accession: A55804
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-300 <K1U>
A:Cross-references: GB:236985; NID:9537421; PID:ell192609; PID:92654382
C:Genetics:
A:Genetic code: SGC5

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C:Keywords: phosphoric monoester hydrolase

Query Match      19.9%; Score 401.5; DB 2; Length 300;
Best Local Similarity 33.0%; Pred. No. 5.1e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;

QY 99 KASVITFGIKGYAEKRGEEEMODAHVILNDITEBCRPSSLITRVSYFAVFDGNGIR 158
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 18 QCKSVIFA---ASEMQGRNTEMDAHIHRHIDQ-----VSFVGFDGNGNE 63

QY 159 ASKFAAQNHLNHLI--RKPRKGDVISEKTVKRCCLDITPKHIDEFL-----KQASSQK 211
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 VAQFEAKHFVDLTKNKNK-----EOKFEAKTEFLKDELLTPEGCKELNOYKA 116

QY 212 AKND-----GSTATCYLAVDNILYIANLGDSPRAITLRYNEESQKHNLSSKEHNPQYEE 267
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 117 TPTDESAYACTANVAGLITKNTLYVANAGDSRSVLCRNNTNH-----DKSVDHKPDNPE 170

QY 268 RMRIQAGGNVNDGRLVLEYSRISIGDQYKRCG-----VTSVPDIRCOLTPNDR 319
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 171 KSRIRAGGFVS DGRVNGVNLNLRALGDLEYKRDKNKLSNEGLIITLAPDVKKTELTPDOK 230

QY 320 FILLACDGLFKVFTPEEAVNFIISLDEKTIOTREGSAADARFEACNRLANKAVQCS 379
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 231 FLLMGCDGVFEFLNHQELKQVNSTIGQAQVTEELLKMAE---DLLDQLLAPDTSQGTG 287

QY 380 ADNVTVNVV 388
   | | | : |
Db 288 CDNMTHITLV 296

RESULT 4
S62462
protein phosphatase 2c homolog 3 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 15-Jun-2001
C:Accession: T38573; S54298; S62462
R:Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: 221745
A:Accession: T38573
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-414 <BA2>
A:Cross-references: EMBL:Z54354; NID:91019398; PIDN:CAA91172.1; PID:91019405; GSPDB:G
R:Shiozaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A:Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase
A:Reference number: S54297; MUID:95163582; PMID:7859738
A:Accession: S54298
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-195, 'T', 197-414 <SH1>
A:Cross-references: EMBL:L34882; NID:9609657; PIDN:AAA67321.1; PID:9609658
C:Genetics:
A:Gene: SPAC2G11.07c
A:Map position: 1L
A:Introns: 110/1; 134/3
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match      18.4%; Score 370.5; DB 2; Length 414;
Best Local Similarity 32.9%; Pred. No. 1.5e-19;
Matches 108; Conservative 53; Mismatches 100; Indels 67; Gaps 13;

QY 81 TSEEEKNGSEELVEKVKVASSVITGLKGYAEKRGEEEMODAHVILNDITEBCRPSS 140
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 10 TEKHSVNSNEP-----VLYGL-----SMQGRNTEMDAHSAL--LSMEC---SA 50

QY 141 LITRVSYFAVFDGNGIRASKFAAQNHLNHLIRK--FKGDVISEKT-----VKRCCLDT 194
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 51 VKDPVDFPFAVVDGNGIRKAVKWCNSNLPQIILEKNDPFOKGFVNALKSSFLNADAKIIDL- 109

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Db 112 FFEVDVSPEASEDEITILE-GVENCLEARRAFFLAD--LALADDCSISTSSGTTALTALV 167
 225 VNDIYINILNIDDSRAILCRYNESQKHAALSLSEKHNPTQYEERMRIKAGGNVDGRVL 284
 Db 168 LGRLLIVANMAGDCRAVLCRKE-----AIDMSQDHRTYSEKRVELGCVYDDGLN 221
 Qy 285 GVLVRSISGDOYK-----RCGVTSPDIRRCQLTPNDRELLACDGLFKVFPPEEAVN 339
 Db 222 GVLVSRAIGMDMKLPKGSASPLISEPELRQIITLEDDEFLICDGIWIDYISSQAVS 281
 Qy 340 FILSLEDEKIQTRGKSAADARYEACNRLANKAVQSGSADNTVMVY 388
 Db 282 IV-----RWGLKRHDDP-EQSAKDLVNEALRRHTIDNLTVIIV 318

RESULT 8

T50783
 protein phosphatase 2C-like protein - Arabidopsis thaliana
 N:Alternate names: protein T30N20_10
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
 C:Accession: T50783
 R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mey
 submitted to the Protein Sequence Database, July 2000
 A:Reference number: 225240
 A:Accession: T50783
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <BEV>
 A:Cross-references: EMBL:AL365234
 A:Experimental source: cultivar Columbia; BAC clone T30N20
 C:Genetics:
 A:Map position: 5
 A:Introns: 27/2; 70/1; 156/1; 185/1; 209/3; 234/3
 A:Note: T30N20_10
 C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 18.1%; Score 364.5; DB 2; Length 348;
 Best Local Similarity 36.4%; Pred. No. 3.2e-19;
 Matches 103; Conservative 47; Mismatches 86; Indels 47; Gaps 13;

Qy 109 GYVAERKGEREMOD-AHVILNDITECRPSSLITRVSYFAVFDGHCIGIRAFKAQNL 167
 Db 35 GY-ASSACKRSSMEDFEFTRIDGINGEI-----VGLCFVFDGHCARAAEYVKRHL 84
 Qy 168 HONLIRKPPKGDVSVETVRCRLDTPFKHDEEFLKQASSQKPAWKD-GSATCVLAVD 226
 Db 85 FSNLT-THPK--FTS--DTKSATIDAYNHTDSELKSENSHN--RDAGSTASTAILVG 135
 Qy 227 NILYIANIGDSRAILCRYNESQKHAALSLSEKHNPTQYEERMRIKAGGNVDGRVLG 286
 Db 136 DLRYVANNGDSRAVSRGK-----ALAVSRDHKPDSDEREKRIENAGCV--MMAGV 186
 Qy 287 LEVRSIDGQYRCGVTSPDIRRCQLTPNDRELLACDGLFKVFPPEEAVNFTLSGLE 346
 Db 187 LAVSAFEDRLKQY-VVADEIDOEKIDTLEFLILASDGLMDFVSEAAVAVY----- 240
 Qy 347 DEKIQTRGKSAADARYEACNRLANKAVQSGSADNTVMVY 389
 Db 241 -----KEVEDP--EDSAKKLVGEAIKRGSDNITCVVR 272

RESULT 9

H96700
 Protein F12A21.5 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96700
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tello
 ker, M.; Wu, D.; Xu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96700
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-464 <SNC>
 A:Cross-references: GB:AE05173; MID:911072032; PIDN:AA628911.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F12A21.5
 A:Map position: 1

Query Match 17.9%; Score 362; DB 2; Length 464;
 Best Local Similarity 29.3%; Pred. No. 7.3e-19;
 Matches 108; Conservative 59; Mismatches 104; Indels 98; Gaps 13;

Qy 102 SVYFLKGY-VAERKGEREMODAHVILNDITECRPSSLITRVSYFAVFDGHCIGIRAS 160
 Db 113 TVSEFGNGFVYVSRNGKKKEMEDTHIV-----PCLVGN--KSFEGYVDGHCAGAKAA 164
 Qy 161 KFAONLHONLIRKPP-KGDVSVETVRCRLDTPFKHDEEFLKQASSQKPAWKDGT 218
 Db 165 EFVAENLHKYVVEEMENCKEKEVE-----AFKAFLRTDPRDFLEKVIKESQLKGAVSG 219
 Qy 219 ATCVLAV--DNILYIANIGDSRAILCRYNESQKHAALSLSEKHNPTQYEERMRIKQ--- 273
 Db 220 ACCVAVAIQDQEMIVSNLGDCAVLCRAG-----VAALTDHDKPGRDDEKERTESQSL 273
 Qy 274 -----AGCNVRD-----GRVLGVLEVRSISGDOYRCGVTSPDIRRCQLTPNDREFI 321
 Db 274 IPFMTFGIÖGCVNDHOGAMKRVQGITLAVSRISGDHLKK-WVAPEPRTVLEBQDMFL 332
 Qy 322 LIACDGLKVPFPPEAVNFTLSCL-----BDEKIQ-----TREG 355
 Db 333 VLASGLMDVYVSNQAVYTVLHLAQRTPKSESEENLVQGVNMSPSKLRASLAVKSP 392
 Qy 356 KSAADARY-----EACNRLANKAVQSGSADNV 383
 Db 393 RCAKSQSYVYNSSENPSPINREIGSSPSKSPITPKSLMAKAAKELANLAKRGSMDDI 452
 Qy 384 TVMVVRIGH 392
 Db 453 TVVITDLNH 461

RESULT 10

T45778
 protein phosphatase 2C-like protein - Arabidopsis thaliana
 N:Alternate names: protein F26013.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 03-Jun-2002
 C:Accession: T45778
 R:Delaney, M.; Berger, C.; Cooke, R.; Grellert, F.; Laurie, M.; Mewes, H.W.; Lemcke, K
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: 223013
 A:Accession: T45778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361
 A:Cross-references: EMBL:AL133452
 A:Experimental source: cultivar Columbia; BAC clone F26013
 C:Genetics:
 A:Map position: 3
 A:Introns: 49/3; 108/3
 A:Note: F26013.110
 C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
 Query Match 17.8%; Score 358.5; DB 2; Length 361;
 Best Local Similarity 30.6%; Pred. No. 9.3e-19;

Tue Jan 21 07:12:51 2003

us-09-935-124a-2.rpr

Page 7

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Oy 1H VERKEEEMNOAHYILNDITBECRPSLLTRSYAVPBGHGIRAKSTAAONJON 170
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 26 LSGMOGRMSMEDHAAILDLD-----NLSFLGVYDGHGKVVSKCAYLHQ 75

Oy 171 LI - RKPKGV - ISEKVVRCILDTFKHTDEEKOA-----206
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 76 VLSDPVAAGDVTSLQKKFF - MDMMGQGRKRELVLGDKINKFSQMEGLMSPR 133

Oy 207 -----SQGR - AM-----KOSTPTCYLAVDNIILITANLGDSPALICRNEQ 249
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 134 SGRSNNKRDAAEEBPSHDFGFGSSGTSCAVARVDQLVYNAAGSKVIL-----SR 187

Oy 250 KHALSLSLKEHNPTQYEEHMRQKAGNVGDGVGLVYSRTSGDQTKRCG-----302
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 188 KQQAATNLSRHKRPLEEAEERLTKAGG IHAGVNSQSLMSRALGDMFERQKKLPSEKQ 247

Oy 303 -VTSVPDTRRCQULTPMDRILTLACDGLFKFTPEEAVNFILSCLEDEKQTQREGSAADA 361
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 248 IYTSAPDVTNVEICDDDDLTLYLACGIGMDQMSQQLVDFIEQLNSE-----T 295

Oy 362 RTEAAGNRLANKAVQGRSA-----DNTVAVVA 389
    :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 296 KLSVYCEKAVLDRCALPNTSGGEGCDNNTMTILVA 328

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Search completed: January 17, 2003, 17:46:10
Job time : 25 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:46 : Search time 14 Seconds

(without alignments)

1161.337 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFGDLPEDPERSPRPAAK.....KAVGRGSDNVTVVVVRIQH 392

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401.5	19.9	300	P2C_PARTE	P49444 paramedium
2	370.5	18.4	414	P2C3_SCHPO	O09173 schizosacch
3	359.5	17.8	454	FEM2_HUMAN	P49593 homo sapien
4	352.5	17.5	434	P2C1_ARATH	P49597 arabidopsis
5	348	17.2	370	P2C2_SCHPO	O09172 schizosacch
6	347	17.2	356	P2C2_CAHEL	P49596 caenorhabd
7	342	16.9	382	P2CA_BOVIN	O62829 bos taurus
8	341.5	16.9	450	FEM2_RAT	O95W77 rattus norv
9	340	16.8	382	P2CA_RABIT	O35814 oryctolagus
10	338	16.7	382	P2CA_RAT	P30650 rattus norv
11	336	16.7	382	P2CA_MOUSE	P49443 mus musculu
12	333	16.5	423	P2C2_ARATH	O04719 arabidopsis
13	326	16.2	390	P2CB_MOUSE	P36993 mus musculu
14	317.5	15.8	390	P2CB_RAT	P35815 rattus norv
15	317.5	15.7	281	P2C1_YEAST	P35182 saccharomyc
16	314	15.6	387	P2CB_HUMAN	O62830 bos taurus
17	313	15.5	479	P2CB_MOUSE	O75688 homo sapien
18	313	15.2	347	P2C1_SCHPO	P40371 schizosacch
19	306	15.1	464	P2C2_YEAST	P49599 arabidopsis
20	305.5	15.1	388	P2C2_ARATH	P49595 saccharomyc
21	303	15.1	491	P2C1_CAHEL	P49595 saccharomyc
22	289	14.9	468	P2C1_YEAST	P49598 leishmania
23	282.5	14.0	399	P2C4_ARATH	O61074 mus musculu
24	281.5	13.5	406	P2C4_MOUSE	P38089 saccharomyc
25	271.5	13.4	542	P2C4_YEAST	P49594 caenorhabd
26	269.5	13.3	393	FEM2_CAHEL	P79126 bos taurus
27	267.5	13.1	449	P2CG_BOVIN	O15355 homo sapien
28	264	12.7	543	P2CG_HUMAN	P49606 ustilaec ma
29	256.5	12.7	546	CYAA_HUMAN	O15297 homo sapien
30	255.5	12.7	2493	P2C1_HUMAN	P35816 bos taurus
31	211.5	10.5	605	P2C1_HUMAN	
32	211.5	10.5	605	P2C1_HUMAN	
33	209	10.4	538	P2C1_BOVIN	

34	209	10.4	598	1	P2CD_MOUSE	O9QZ67 mus musculu
35	208	10.3	2300	1	CYAA_NEUR	O01631 neurospora
36	207	10.3	538	1	P2C1_RAT	O88483 rattus norv
37	206	10.2	1839	1	CYAA_SACCL	P23486 saccharomyc
38	204.5	10.1	383	1	P2C4_SCHPO	O14156 schizosacch
39	203	10.1	581	1	P2C4_SCHPO	O9P011 homo sapien
40	202	10.0	581	1	KAPF_ARATH	P46014 arabidopsis
41	194	9.6	529	1	P2C2_HUMAN	O96219 homo sapien
42	188	9.3	530	1	P2C2_RAT	O88484 rattus norv
43	185.5	9.2	2026	1	CYAA_YEAST	P08678 saccharomyc
44	178	8.8	504	1	TA61_HUMAN	O15750 homo sapien
45	178	8.8	2145	1	CYAA_PODAN	O01513 podospira a

ALIGNMENTS

RESULT 1	ID	P2C_PARTE	STANDARD:	PRT:	300 AA.
AC	P49444:				
DT	01-FEB-1996 (Rel. 33, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Protein phosphatase 2C (PP2C).				
OS	Paramedium tetraurelia.				
OC	Paramedium tetraurelia.				
OC	Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Penicillida:				
OX	NCBI:taxid:5888;				
RN	(1)				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RC	STRAIN-51S;				
RX	MEDLINE-95105156; PubMed-7806499;				
RA	Kiump S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,				
RA	Pinna L.A., Schultz J.E.;				
RT	"A membrane-bound protein phosphatase type 2C from Paramedium				
RT	tetraurelia. Purification, characterization, and cloning."				
RL	J. Biol. Chem. 269:32774-32780(1994).				
CC	- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.				
CC	- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +				
CC	phosphate.				
CC	- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).				
CC	- SUBCELLULAR LOCATION: Membrane-bound.				
CC	- PTM: THE N-TERMINUS IS BLOCKED.				
CC	- SIMILARITY: BELONGS TO THE PP2C FAMILY.				
CC	-				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
DR	EMBL: Z36985; CA85448.1; -				
DR	HSSP: P35813; IM6Q.				
DR	InterPro: IPR001932; PP2C-like.				
DR	InterPro: IPR002222; PP2C.				
DR	Pfam: PF00481; PP2C; 1.				
DR	SMART: SM00331; PP2C_SIG; 1.				
DR	SMART: SM00332; PP2C; 1.				
DR	PROSITE: PS01032; PP2C; 1.				
KW	Hydrolyse; Magnesium; Manganese; Membrane.				
FT	METAL 37				
FT	METAL 38				
FT	METAL 57				
FT	METAL 237				
FT	METAL 289				
SO	SEQUENCE 300 AA; 33739 MW; BC0318BAFF7724EC CRC64;				

Query Match 19.9% Score 401.5; DB 1; Length 300;
Best Local Similarity 33.0%; Pred. No. 7.3e-22;
Matches 102; Conservative 53; Mismatches 105; Indels 49; Gaps 9;


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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
DE (CAMKase) (hFEM-2).
CN KIAA0015
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OK NCBI_TaxID=9606;
RN
  [1]
  RP SEQUENCE FROM N.A.
  RP PubMed=11559703;
  RA Tan K.M.L., Chan S.L., Tan K.O., Yu V.C.;
  RT "The Caenorhabditis elegans sex-determining protein fem-2 and its
  RT human homologue, hFEM-2, are Ca2+/calmodulin-dependent protein kinase
  RT phosphatases that promote apoptosis."
  RL J. Biol. Chem. 276:44193-44202(2001).
  [2]
  RP SEQUENCE FROM N.A.
  RP TISSUE=Bone marrow;
  RX MEDLINE=96051387; PubMed=7584026;
  RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawabayashi Y.,
  RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
  RT "Prediction of the coding sequences of unidentified human genes. I.
  RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
  RT analysis of randomly sampled cDNA clones from human immature myeloid
  RT cell line KG-1."
  RL DNA Res. 1:27-35(1994).
  [3]
  CC -1- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
  CC kinase II activated upon autophosphorylation, and CAM-kinases IV
  CC and I activated upon phosphorylation by Cam-kinase kinase.
  CC Promotes apoptosis.
  CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
  CC phosphate.
  CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
  CC -1- SUBUNIT: Associates with Filafila.
  CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
  CC -----
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  CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  CC or send an email to license@isb-sib.ch).
  CC -----
  DR EMBL: AF305840; AAL15579.1; .
  DR EMBL: D13640; BAA02803.1; .
  DR InterPro: IPR001932; PP2C-like.
  DR InterPro: IPR000222; PP2C.
  DR Pfam: PF00481; PP2C_1.
  DR SMART: SM00331; PP2C_SIG_1.
  DR SMART: SM00332; PP2C_1.
  DR PROSITE: PS01032; PP2C_1.
  KW Hydrolyase; Magnesium; Apoptosis; Multigene family.
  FT DOMAIN 101 107 POLY-Clu
  FT METAL 360 360 MANGANESE 2 (BY SIMILARITY).
  FT METAL 404 404 MANGANESE 2 (BY SIMILARITY).
  FT CONFLICT 202 202 D -> G (in Ref. 2).
  SQ SEQUENCE 434 AA; 49888 MW; 2A36262331BC9CF CRC64;
  Query Match 17.8%; Score 359.5; DB 1; Length 454;
  Best Local Similarity 28.1%; Pred. No. 1.3e-18;
  Matches 126; Conservative 65; Mismatches 145; Indels 111; Gaps 16;
  Oy 10 PERSPRAGKRNKQPL-LPDDLPASSTDSGSGPPLFLFDLPASSGD-----SG 60
  Db 6 POKSSPMASCAETPGFDLTLDLPALNPE-----DPLPWKAPVLSQEEVEG 56
  Oy 61 SLA-----TSISQVXTE-----GKCAKRTSEERKNSSEIVE 94
  Db 57 ELAEFLMGFLGSRKAPPLAALAHAEVVSOLQTLDSFRRKLPREEEEDDDDEEKAP 116

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Oy 95 KVCVASSVTEGLKGYAERKE-----REEMOAHNL 128
Db 117 VTLDAQSLAOSFPNRLMEYAGQOKVPLAARASQOMLVSHAIRNRRMEERVSL 176
Oy 129 NDITECPSPSSLTIRVSTFAVFDHGIRASKEPAONLHONLIR-----EPKGDVSEV 183
Db 177 PSF-NQLFGSDPVNR-AFPAVFDGVDGDAARAAVHTNAARPELPTPEE-- 229
Oy 184 EKYVRCLDTEFKHTDEEPLKQASSOKPAMKDGSTATCVLAVNITYIANLDSRAILCR 243
Db 230 -----ALREAFRRITDMLFRKRRER--LQGTGVCALIAAGATLHVAMLDSQVILV- 280
Oy 244 YNEESQKHAALSLSEKHNPTOYERMRLOKAGNVRD-----GRVLGVLEVSRSIGQYKR 300
Db 281 -----QOQOVYKMLPEPRERODEKARIEALGEGVSHMDQWRNGTLAVSRAIGD-VFOK 334
Oy 301 CGVTSVPPIRRCOTPDNRFILACDGLFEKVFTEPEAVNFTLSCLDEKIQTRGKSAD 360
Db 335 PYVSGEADDAARALTGSEDTLLIACDGFDPVPHQEVVGLVQSHL-----TRQGSGLR 388
Oy 361 ARYEACNRLANRKAIVORGADNVYVWV 388
Db 389 VAE-----LVAAAREGSHDNTVWV 411
RESULT 4
P2CL ARATH STANDARD: PRT: 434 AA.
AC P49557;043717; 094C87;
DT 01-FEB-1996 (Rel. 33, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2c AB11 (EC 3.1.3.16) (PP2C) (abscisic acid-
DE insensitive 1).
DE AB11 OR AY4G26080 OR F20B18.190.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN
  [1]
  RP SEQUENCE FROM N.A. AND VARIANT ASP-180.
  RP STRAIN=cv. Landsberg erecta;
  RX MEDLINE=94255767; PubMed=8197457;
  RA Meyer K., Leube M.P., Grill E.;
  RT "A protein phosphatase 2c involved in ABA signal transduction in
  RT Arabidopsis thaliana."
  RL Science 264:1452-1455(1994).
  [2]
  RP SEQUENCE FROM N.A.
  RP STRAIN=cv. Columbia; TISSUE=leaf;
  RX MEDLINE=95007758; PubMed=7923358;
  RA Mindinos M., Katagiri F., Yu G.L.,
  RT "The A. thaliana disease resistance gene PR2 encodes a protein
  RT containing a nucleotide-binding site and leucine-rich repeats."
  RL Cell 78:1089-1099(1994).
  [3]
  RP SEQUENCE FROM N.A.
  RP STRAIN=cv. Columbia; TISSUE=leaf;
  RX MEDLINE=94255766; PubMed=7910981;
  RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Cheffor F.,
  RA Giraudat J.;
  RT "Arabidopsis ABA response gene AB11: features of a calcium-modulated
  RT protein phosphatase."
  RL Science 264:1448-1452(1994).
  [4]
  RP SEQUENCE FROM N.A.
  RP STRAIN=cv. Columbia;
  RX MEDLINE=20083480; PubMed=10617198;
  RA Mayer K.F.X., Schueller C., Wambut R., Murphy G., Voicakart G.,
  RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
  RA Harris B., Ansdorge W., Brandt P., Grivell L.A., Rieger M.,

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RA Wehlselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreits M., Delany M., Pulgomech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohlseil J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandebussche F.,
RA Braeken M., Melijens I., Voet M., Bastiaens I., Aert R., Delcor E.,
RA Weitzenegger T., Botne G., Ramsperger U., Hilbert H., Braun M.,
RA Hölzer E., Brandt A., Peters S., van Staveren M., Dirksen W.,
RA Moorjman P., Klein Lankhorst R., Rose M., Hauf J., Koester P.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysbaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., Mcclay K., Mayes R.,
RA Parlett A., Rajandream M.A., Lyne M., Benes V., Reckmann S.,
RA Borfova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Danner D., Herzl A.,
RA Neumann S., Argitlioni A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Mendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chetoui F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Purrelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleike C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Haebmann K.,
RA Parrell L., Desha N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Storelle P., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Clout J., Abbott A., Scott K., Johnson D.,
RA Mlin P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kremer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Speith J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vill D., Shekhar M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Chen E., Marra M., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA "Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*."
RT Nature 402:769-777(1999).
RL
RN
RP
RC
RA STRAIN=cv. Columbia;
RA Shiozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN ABSICISIC ACID (ABA) SIGNALING PATHWAY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC
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CC
CC EMBL: X78886; CAA55484.1; -;
CC EMBL: U12856; AAA50237.1; -;
CC EMBL: X77116; CAA54383.1; -;
CC EMBL: AL049448; CAB39673.1; -;
CC EMBL: AL161564; CAB79463.1; -;
CC EMBL: AY035073; AAK59578.1; -;
CC HSSP: P35813; IAOO.
CC InterPro: IPR002048; EF-hand.
CC InterPro: IPR001932; PP2C-like.

DR InterPro: IPR002022; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C-StG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS00018; EF-HAND; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydrolyase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT CA_BIND 93 104 EF-HAND (POTENTIAL).
FT DOMAIN 417 420 POLY-VAL.
FT VARIANT 180 180 G->D (MILKY PHENOTYPE AND ABA-
FT CONFLICT 24 24 G->R (IN REF. 5).
FT CONFLICT 105 105 I->V (IN REF. 1).
SQ SEQUENCE 434 AA: 47505 MW: 444C54F04195F572 CRC64;
Query Match 17.5%; Score 352.5; DB 1; Length 434;
Best Local Similarity 29.4%; Pred. No. 3.9e-18;
Matches 125; Conservative 65; Mismatches 148; Indels 87; Gaps 19;
QY 2 DLFGDLPEPER-SPRPAKGEAKGFLPDDLPASSTDSGGGFLPDP-PPASG- 58
DB 45 DLWVSLPEVSSGVSSGSHSESRKVLISRNPNLMKESAADIYVD-LSNG- 100
QY 59 SGSLATSIQWY-KTEGKAKKRTSEEEKNGSEELVEKVKVCAASYIFGLKGVAE- 117
DB 101 NCSDTISEKKMISRT- - - - -SRSLFEFK- - - - -SVPLYGFTSIC- - - - -SR 137
QY 118 REMEDAHYLLNDIEECRPSSLI- - - - -TRSYVAFVDFGGRIRASKFAFAN- 169
DB 138 REMEDA- - - - -VSTIPREFLOSSSGMLDRFPDQSAAHFVGVDHGGSVAVCR- 194
QY 170 NLIRKPK- - - - -GDVISEVETVRKCLLDTEFKTDEEFLQASSOKPAMKDGST- 222
DB 195 ALAEELAKKPKMLCGDT- - - - -WLEKM- - - - -KKAFLNPLRVDSIESVAPETV- - - - -GRTS 247
QY 223 LAVNDILTYANIGDSRAILCRNIESQKHAALSLEHNPTQYEEBMRIOKAGNV- 279
DB 248 VVFPSTHIFPANGDSRAVLCR- - - - -GKTALPLVDHPRDEDEARLEAAGKAT- 301
QY 280 DRRVLGVLEFVSISIGDGYKRCGVTSVPDIRCOLTPNRFILLCDDGLFKVFTPEAVN 339
DB 302 GARVGVLAAMSISIGD-RLKPSIIPDPVTVAKRKEDDCILASDGVMDVMTDEACE 360
QY 340 FI- - - - -ISCLEDEKIQTEGKSADARVEACNRKANAVQSGADNV 383
DB 361 MARKRILLHKKKNVAVAGDSLADLER- - - - -RKEGK- - - - -DPAAMSAEVLSKLAIGRSKONI 415
QY 384 TYMNV 388
DB 416 SVVV 420
RESULT 5
PC22_SCHPO STANDARD: PRT; 370 AA.
AC 009172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN PTC2 OR SPC123.11.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN
RP
RC STRAIN=972;
RX MEDLINE=95163582; PubMed=7859738;
RA Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
kinase kinase homolog in the osmoregulation of fission yeast.";

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RL EMBL J. 14:492-502(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972:
RX MEDLINE-21848401; PubMed-11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Soutos J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
RA Goble A., Goble A., Hamlin N., Harris D., Hidalgo T., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor R., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymptre B.,
RA Meljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Filiz C., Holtzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambolt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez J., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,
RA Cerutti L., Lowe T., McComb W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Ussey D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
CC SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOREGULATING SIGNAL
CC TRANSMITTED THROUGH WIS1 MAP KINASE.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L34881; AAA67320.1; -.
DR EMBL: AL031579; CAA20880.1; -.
DR HSSP: P35813; 1A6Q.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C_Sig; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydrolyase; Magnesium; Manganese; Multi-subunit.
FT METAL 37 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 39 MANGANESE 1 (BY SIMILARITY).
FT METAL 63 64 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 253 254 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 283 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 283 MANGANESE 2 (BY SIMILARITY).
SQ
SEQUENCE 370 AA: 40878 MW: DBDDB826FA40AC50 CRC64:
Query Match 17.28; Score 348; DB 1; Length 370;
Best Local Similarity 32.58; Pred. No. 6,7e-18;
Matches 98; Conservative 47; Mismatches 103; Indels 54; Gaps 12;
QY 111 VAEKGEREMODAHVIINDITE--ECRPSSLITFVSFAFVFDGHCIGRASKFAQNHL 168
DB 26 VSHMOGRISMEDAHCALINFTDSSNSNPPT-----SFGVFDHGSDGRVAKYKCRHL- 78

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QY 169 QNLRKPP---KGDVISEKTVKRLDTEFKHTDEEFLKASSOKPAMKDSATVCYLA 225
DB 79 PDIIKSPSFWKGN-----YDEALKSGFLAANALMODRMOED--PSGCTATYLAIV 129
QY 226 DN-ILYIANIGDSRAILCRYNESQHAALSLEKHNPTQYEERMIOKAGVNDRCYL 284
DB 130 DHOYICANMGDSRTVLGR-----KGTAEPLSDHFPNNVDYKARITFAAGFIDFGVN 183
QY 285 GVLVSRSTIGDQYKRCG-----VTSVPDIRCQLFPNDFILACDGLFVTFPPE 336
DB 184 GSLASRAIDPEFKKDSLPPEKQIVTAFPDVYIHNIDPDDFLILACDGIWCKSSQ 243
QY 337 AVNITLSCLEDEKIQIREKSAADARPAACNRLANKAVRG-----ADNYVMYRI 390
DB 244 VEEV-----RGIYARQS-LEVICENIMDCIASNESGICGDMITICIVAF 291
QY 391 GH 392
DB 292 LH 293

```

```

RESULT 6
P2C2_CAEEL STANDARD; PRT: 356 AA.
ID P2C2_CAEEL
AC P49596;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein phosphatase 2C T23P11.1 (EC 3.1.3.16) (PP2C).
GN T23P11.1
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Chordata; Rhabdillidae; Rhabdillidae;
OC Rhabdillidae; Polioptila; Caenorhabdillidae.
OX NCBI-TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Swaburne J.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RA DUBIN R.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Z46343; CAA86456.2; -.
DR HSSP: P35813; 1A6Q.
DR WormPeP: T23P11.1; CE24009.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C_Sig; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hypothetical protein; Hydrolyase; Magnesium; Manganese.
FT METAL 37 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 39 MANGANESE 1 (BY SIMILARITY).
FT METAL 58 59 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 228 229 MANGANESE 2 (BY SIMILARITY).
FT METAL 277 278 MANGANESE 2 (BY SIMILARITY).
SQ
SEQUENCE 356 AA: 39064 MW: EDCB0841CFB026B5 CRC64:

```

Query Match	17.2%	Score 347	DB 1	Length 356	
Best Local Similarity	31.4%	Pred. No. 7.5e-18			
Matches 101	Conservative	57	Mismatches 106	Indels 56	Gaps 12

QY	91	ELVEKKVCKASSVIFGLGVAAE---RKGEREMODAHVILNDITECRPPSLITRVS	147
Db	3	QTLSEPIIRKKESASCANENYLVGSSCMQGWIRDMEDATHHLLSLDD-----PKCAF	54
QY	148	FAVEDGHGICIRASKTAOONLHONLI--RKPKGDV--ISYEKTVKRCLLDTFKHTEDEFIK	204
Db	55	FAVYDGHGSKSVQSGIHLHKVVAOKFEFSGNKKAEIKEFLE--LDOQMRVDEETKD	112
QY	205	QASSCKPAMKQSGSTATCYLANDNLIYINIGDSRAILICRYNESQKHALSLSKENHPQ	264
Db	113	DVS-----GTTAAVVLLIKEGDVYCGNAGSGRAVSSVGE-----ARPLSFHKPSS	158
QY	265	YEERMRIQACGANNVDGRLVGLVEVRSRISGDQYKRCG-----VTSVPDIRCOLTP	316
Db	159	ETEARRIITIAAGGWFENRNVGNLSTRALGDAFRFNCDTPKAEBOIVTAFPRVITDKLTP	218
QY	317	NDRFILLACDGLFKVYFTPEEAVNFTLSCLEDEKIQTRGKSSAADARYEAACNRLANKAV	375
Db	219	DHEFTVLACDGIIMDVMTNQEVVDV-----RE-KLAERKRDPOSICBELLTRCLA	266
QY	376	---QRG--SADNVTVYVVRIGH	392
Db	267	PDCQMGGLGCDNMIVVLGLLH	288

```

RESULT 7
P2CA_BOVIN
ID P2CA_BOVIN STANDARD: PRI: 382 AA.
AC 062829;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha).
GN Pp1A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98146173; PubMed=9486768;
RA Klump S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
RT "Protein phosphatase type-2C Isozymes Present in Vertebrate Retinae:
RT Publication, Characterization, and Localization in Photoreceptors.";
RL J. Neurosci. Res. 51:328-338(1998).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
CC DR EMBL; AJ005457; GCA06554.1; -.
CC DR HSSP; P35813; 1A60.
CC DR InterPro; IPR001932; PP2C-like.
CC DR InterPro; IPR000222; PP2C.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_STG; 1.
CC SMART; SM00332; PP2C; 1.

```

Query Match	Score	DB 1:	Length
Best Local Similarity	33.7%	Pred. 101	Indels 48; Gaps 12
Matches 101; Conservative	47;	Mismatches 104;	

QY 106 GLKGVYERGEREMODAYLINDITEEORPSSLTIRSYAVEGHGCIASFAAQ 165
 Db 21 GLRGJSSMGQWRREMDAHTAVIGL-----PSGLFT-MSFAVYDGHGSOVAKCE 73
 QY 166 NLHONLIRKRP-KCD--VISVETVKRCLLDTEKHNDEFLKQASSOKPAMKDGSTATCY 2222
 Db 74 HLDHITNNODFKDSAGAPSYE-NVKNGIIRTGFELEIDHNRYVSEKKGHDGSGTAVGV 1322
 QY 223 LAVDNILYIANLGSRAILICRYNEESQKHAALSKEHNTOYEERRIORKAGNVRDGR 2822
 Db 133 LISQHTYFLINCDSRCLLR-----NRKYPTTDHAKRSNPLEKRIIONAGGSVAIQR 1666
 QY 283 VLGVLEVRSIGDQYKRC---GVY-----SYVDIRCOLTPNDRIILLACDGLFK 3300
 Db 187 VNGSLAVSRALGDGDYK-CHGKGPTQLVSPPEVHDIRSE--EDDOCFILACDGIWD 2433
 QY 331 VFPPPEAVNFLSTLE-DEKIORREKSAADARYEAALANKAANORASANNVPMYV 3688
 Db 244 VMGNBEELCDPVRKSLVETDD-----LEKVCNEVDVTCILYKSSRDMWSVILI 2899

RESULT 8			
FEM2_RAT			
ID	FEM2_RAT	STANDARD:	PRT: 450 AA.
AC	Q9WVR7		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)		
DE	(Cam-kinase phosphatase) (CamKpase).		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=99279559; PubMed=10348902;		
RA	Kiliani T., Ishida A., Okuno S., Takeuchi M., Kameshita I.,		
RA	Fujisawa H.;		
RT	"Molecular cloning of Ca2+/Calmodulin-dependent protein kinase		
RT	phosphatase."		
RL	J. Biochem. 125:1022-1028(1999).		
CC	-1- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-		
CC	kinase II activated upon autophosphorylation, and Cam-kinases IV		
CC	and I activated upon phosphorylation by Cam-kinase kinase.		
CC	Promotes apoptosis.		
CC	-1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +		
CC	phosphate.		
CC	-1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).		
CC	-1- SUBUNIT: Associates with Flialpha (By similarity).		
CC	-1- SIMILARITY: BELONGS TO THE PR2C FAMILY.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC EMBL: AB023634: BAA82477.1:
DR InterPro: IPR000222: PP2C-
DR InterPro: IPR001932: PP2C-like.
DR Pfam: PF00481: PP2C: 1.
DR SMART: SM00332: PP2C: 1.
DR SMART: SM00331: PP2C-Stg: 1.
DR PROSITE: PS01032: PP2C: 1.
KW Hydroxylase; Magnesium; Manganese; Apoptosis; Multigene family.
FT DOMAIN 99 109 POLY-GLU.
FT METAL 356 356 MANGANESE 2 (BY SIMILARITY).
FT METAL 400 400 MANGANESE 2 (BY SIMILARITY).
SQ SSOURCE 450 AA: 49165 MW: 67626542F32BAFDD CMC64;

Query Match 16.9%; Score 341.5; DB 1; Length 450;
Best Local Similarity 29.4%; Pred. No. 2.5e-17;
Matches 124; Conservative 63; Mismatches 160; Indels 75; Gaps 16;

QY 3 LFQDLPEPRSPRPAAGKEAKGFLFDLPPASSTDSGGGFLFDLPPASSGDSGL 62
DB LLDQFPAPLSESLPMK-VPGTVLQGEVEAELETAMGF-LGSRAAPPVAV-AAVT 79
QY 63 ATSIQWVTEGKAKRKTSSEKNGSEE-----LVKK-----VCKASVY 104
DB HEALISQLOTDLSEFKRLPEGEDEEEERVLTLDKGLSRFFCMLNCSQMKR 139
QY 105 FGKGVYAEK-----GEEMODAHVILNDTECRPSLLTRVS-----YFA 149
DB 140 VPLTAQAPQRKLVSIHAIKTRKMKEDRVSL-----PAFNLHGLSDSVHRAIF 191
QY 150 VFDGCGITASKFAAONHONLIRKPKGVISEVETVRCLLDTFKTDEELKQASSO 209
DB 192 VFDGCGVDAAKRAVSHVHTNASHO-PE-----LTDPAAALKEAFRTDDMFLOKKRE 245
QY 210 KPAKDCSTATCVLAVNDILYIANLGDRAILICRYNESQKHAALSLSKHNPTQYEER 269
DB 246 R-LOGGTTGVCALLTGAALHVAWLGDQVYL-----QCGQVVKMEPRKRODEK 297
QY 270 RIGKAGNVR--DSRVGLVLEVSRTIGDQYRCQVTSVPDIRCQLTPNDRILLACD 326
DB 298 RIALGFGVSLMDCKRVNGTGLAVSRAIG-VFQKPYVSEADMAARELTGLEDILLACD 356
QY 327 GLFKFVTPREAVNFTLSCLDEKIQTRREGKSADARYEACRLANKAVQGSADNTVAV 386
DB 357 GFEDVVRHHEIRGLVHGLHRLQK--GSGMHVAE-----ELVAVARDGSHDNITVM 405
QY 387 VV 388
DB 406 VV 407

RESULT 9
P2CA_RABIT STANDARD: PRT: 382 AA.
AC P35814;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein Phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92182001; Pubmed=1311954;
RA Mann D.J., Campbell D.G., McCowan C.H., Cohen P.T.W.:
RA "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RT comparative analysis of amino acid sequences."
RL Biochim. Biophys. Acta 1130:100-104(1992).
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CC -1- FUNCTION. ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL: S87757; AAB21763.1:
DR PIR: S22422; S22422.
DR HSSP: P35813; 1A60.
DR InterPro: IPR001932: PP2C-like.
DR InterPro: IPR000222: PP2C.
DR Pfam: PF00481: PP2C: 1.
DR SMART: SM00331: PP2C-Stg: 1.
DR SMART: SM00332: PP2C: 1.
DR PROSITE: PS01032: PP2C: 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 382 AA: 42462 MW: 468CF1854FDC486 CRC64;

Query Match 16.8%; Score 340; DB 1; Length 382;
Best Local Similarity 33.7%; Pred. No. 2.6e-17;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLKGVYAEKREEMODAHVILNDTECRPSLLTRVSYFAVDEGGIGIRASKFAAQ 165
DB 21 GLRYGLSLMSGWRWEMEDAHVATIGL-----PSGLEF-WSFAVYVDGAGSQVAKYCE 73
QY 166 NLHONLIRKRP-KGD--VISVEKTVRCLLDTFKTDEELKQASSQKPAWMDGSTAVCY 222
DB 74 HLLDITINQDFKSGAGPSVE-NVKNIGIRGTGLEIDHHRVSEKKHGADRSSTAVGV 132
QY 223 LAVNDILYIANLGDRAILICRYNESQKHAALSLSKHNPTQYEEMRIQKAGVWRDGR 282
DB 133 LISPGHTYFINCGDSRGLCR-----NRKVHFTQDHKPSNLEKRIQNNAGSVMIQR 186
QY 283 VIGVLEVSRTIGDQYRCQVTSVPDIRCQLTPNDRILLACDGLFK 330
DB 187 VNGSLAVSRALGDPDYK-CYHGKGPTEBOLVSPPEVDIERSE--EDDPITILLACDGLMD 243
QY 331 VFTPEAVNFTLSCLF--DEKIQTRREGKSADARYEACRLANKAVQGSADNTVAVV 388
DB 244 VNGEELCDIFVRSKLEYTD-----LEKVCNEVDYDCLVYKGSNDMSVILI 289

RESULT 10
P2CA_RAT STANDARD: PRT: 382 AA.
AC P20650;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A OR PP2C1.
OS Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
```


AC p35813.075551.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2c alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
GN (Protein phosphatase 1A).
GN PPMA1 OR PPMA1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId:9606;
RN [1]
RX SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RX MEDLINE:92182001; PubMed:1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RA Takekawa M., Maeda T., Saito H.;
RA "Protein phosphatase 2calpha inhibits the human stress-responsive p38
and JNK MAPK pathways.";
RL EMBO J. 17:4744-4752(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RP TISSUE-Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE:97157470; PubMed:9003755;
RA Das A.K., Helms N.R., Cohen P.T.W., Barford D.;
RA "Crystal structure of the protein serine/threonine phosphatase 2C at
2.0 Å resolution.";
RL EMBO J. 15:6798-6809(1996).
RT 1. FUNCTION: Enzyme with a broad specificity.
RT 1. CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
phosphate.
CC 1. COFACTOR: Binds 2 magnesium or manganese ions.
CC 1. SUBUNIT: MONOMER.
CC 1. ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC 1. SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL: S87759; AAB21784.1; -;
DR EMBL: AF070670; AAC28354.1; -;
DR EMBL: BC026691; AAH26691.1; -;
DR PIR: S22423; S22423.
DR MIM: 606108; -;
DR GENE: HGNC:9275; PPMA1.
DR PDB: 1A60; 27-MAY-98.
DR InterPro: IPR001932; PP2C-1like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C-SIG. 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KM Hydrolyase; Magnesium; Manganese; Multiene family;
KM Alternative splicing; 3d-structure.
FT METAL 37 37 MANGANESE 1.
FT METAL 38 38 MANGANESE 1.
FT METAL 60 60 MANGANESE 1 AND 2.
FT METAL 239 239 MANGANESE 2.

CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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CC -----
DR EMBL: Y08966; CAA70163.1; -
DR EMBL: Y08965; CAA70162.1; -
DR EMBL: Y11840; CAA72538.1; -
DR EMBL: AB024035; BAA97035.1; -
DR HSSP: P35813; 1A6Q.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00331; PP2C_SIG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT SEQUENCE 423 AA; 46306 MW; 67CAAC76DA531A71 CRC64;

Query Match 16.5%; Score 333; DB 1; Length 423;
Best Local Similarity 29.3%; Pred. No. 9.5e-17;
Matches 118; Conservative 63; Mismatches 130; Indels 92; Gaps 19;

QY 51 LPPAS-SDSG-----SLATISQMTVEGKGARKRKSEKKNSEEL----- 92
DB 34 LPSSCSGDGAMKSDSFETNRQDSLTTSSSSAMAGVD-----ISAGEINSGSDEFDPSS 87
QY 93 ---VKKRYCK--ASSVIFGLKGY---VAERKGEREMOD-----AVILIND 130
DB 88 MNQSKKRLSRRESRLFEKFCVPLGYTSICGRPEMEDSVTIPRLQVSSSLDOR 147
QY 131 ITEECRPSSLLTRVSYFAVEDGHGIRASKFAQNLH---QNLIRKFPK---GDVTSV 183
DB 148 VTNGCFPHLS---AHFGVYDGHGSGQVANCYRERHMLALTEIEVKEPECDGD--TW 201
QY 184 EKVYRCLDTFFKHTDEFELKQASQKPAKMDGSTATCVLANDLNLIYANLDSRAILCR 243
DB 202 QEKMKALFNSFMVRDSELETVAHAPETV---GSTSVAAVFPPTHIFVANCDSRAVLCR 258
QY 244 YNEESQKHAALSLSKEHNPTQYEERMRIQKAGNV---RDGVLVGLEVRSRIGGOYKR 300
DB 259 -----GTPPLALSYDHNPRDDEAKRIEAGKVIIRNNGARVFGVLAISRIGD-RYIK 311
QY 301 CGVTSVPDIRCQLTPNDRFILLACDGLFKYFTPEAVNF---IL-----SCL 345
DB 312 PSVIPDPPEVTSVRVKEDDCLTLASDGLMDVMTNEVCDLARKRILLMHKKNAMAGEALL 371
QY 346 EDEKIQTRGKSAADARYEACNRKANAVORGSDANTVAVVY 388
DB 372 PAEK--RGECK---DPAAMSAEYLSKMALOKSGKDNISVVVY 409

RESULT 14
P2CB_MOUSE STANDARD: PRT; 390 AA.
ID P2CB_MOUSE
AC P36593;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
DE (Protein phosphatase 1b).
GN PPM1B OR PPM1B OR PP2C2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [3]

RP SEQUENCE FROM N.A.
RX MEDLINE=94099616; Pubmed=8274020;
RA Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
RA Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.;
RT "Molecular cloning of a novel isoform of Mg(2+)-dependent protein
RT phosphatase beta (type 2C beta) enriched in brain and heart.";
RL Arch. Biochem. Biophys. 307:342-349(1993).
RN [2]
RP SEQUENCE FROM N.A. (BETA-3, BETA-4 AND BETA-5).
RC TISSUE-Testis.
RX MEDLINE=95251388; Pubmed=7733667;
RA Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
RA Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.;
RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein
RT phosphatase beta-4 (type 2C beta-4)." ;
RL Arch. Biochem. Biophys. 318:387-393(1995).
RN [3]
RP SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
RC TISSUE-Testis.
RX MEDLINE=94313028; Pubmed=8038726;
RA Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
RT "Molecular cloning and expression of cDNAs encoding two isoforms of
RT protein phosphatase 2C beta from mouse testis.";
RL Biochem. Mol. Biol. Int. 32:773-780(1994).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv.
RX MEDLINE=99398339; Pubmed=10469137;
RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
RA Yanagawa Y., Kusuda K., Hiraga A., Tamura S.;
RT "Alternative promoters direct tissue-specific expression of the mouse
RT protein phosphatase 2Cbeta gene." ;
RL Eur. J. Biochem. 263:736-745(1999).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O -> a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS, BETA-1 (SHOWN HERE), BETA-2,
CC BETA-3, BETA-4 AND BETA-5. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC THEY ONLY DIFFER IN THEIR C-TERMINUS.
CC -1- TISSUE SPECIFICITY: BETA-1 IS EXPRESSED UBIQUITOUSLY; BETA-2 IS
CC EXPRESSED EXCLUSIVELY IN BRAIN AND HEART; BETA-4 IS EXPRESSED
CC EXCLUSIVELY IN BRAIN AND INTESTINE; BETA-3 AND BETA-5 ARE
CC EXPRESSED EXCLUSIVELY IN TESTIS AND INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D17411; BAA04233.1; -
DR EMBL: D17412; BAA04234.1; -
DR EMBL: D45859; BAA08293.1; -
DR EMBL: D45860; BAA08294.1; -
DR EMBL: D45861; BAA08295.1; -
DR EMBL: U09218; AAB60442.1; -
DR EMBL: AB007798; BAA84471.1; JOINED.
DR EMBL: AB007794; BAA84471.1; JOINED.
DR EMBL: AB007795; BAA84471.1; JOINED.
DR EMBL: AB007796; BAA84471.1; JOINED.
DR EMBL: AB007797; BAA84471.1; JOINED.
DR PIR: S39780; S39780.
DR HSSP: P35813; 1A6Q.
DR MGD: MGI:101841; Ppm1b.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00331; PP2C_SIG; 1.

Search completed: January 17, 2003, 17:44:11
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:46 ; Search time 35 Seconds

(without alignments)
2307.728 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018

Sequence: 1 MDLFGDLPPEPERSPPACK.....KAVRGSDNVTVMVVRIQH 392

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacterioplasmid:*
17: SP-archaeoplasmid:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	4 Q9H0C8	Q9H0C8 homo sapien
2	1935	95.9	392	1 Q9H0F6	Q9H0F6 mus musculu
3	1931	95.7	392	11 Q9Z1Z6	Q9Z1Z6 rattus norv
4	1386	68.7	272	11 Q9DC99	Q9DC99 mus musculu
5	1078	53.4	212	11 Q9CS46	Q9CS46 mus musculu
6	856	42.4	167	11 Q9Z0T2	Q9Z0T2 mus musculu
7	481	23.8	351	10 Q9LMT1	Q9LMT1 arabidopsis
8	480	23.8	351	10 Q944K0	Q944K0 arabidopsis
9	474	23.5	242	5 Q62212	Q62212 caenorhabdi
10	408.5	20.2	319	10 Q8S8Z0	Q8S8Z0 mesembryant
11	398.5	19.7	311	10 Q8RXV3	Q8RXV3 arabidopsis
12	381.5	18.9	243	10 Q8S3P1	Q8S3P1 oryza sativ
13	368.5	18.3	420	10 Q8VZD6	Q8VZD6 arabidopsis
14	368	18.2	389	10 Q81773	Q81773 arabidopsis
15	368	18.2	975	5 Q15743	Q15743 dicystostei
16	366.5	18.2	420	10 Q94AT1	Q94AT1 arabidopsis

17	366.5	18.2	757	4 Q9UPR0	Q9UPR0 homo sapien
18	365	18.1	359	10 Q8Z4D9	Q8Z4D9 mesembryant
19	365	18.1	766	4 Q8WT54	Q8WT54 homo sapien
20	364.5	18.1	348	10 Q9LEW5	Q9LEW5 arabidopsis
21	364.5	18.1	371	10 Q8VZM9	Q8VZM9 arabidopsis
22	362	17.9	464	10 Q9FXE4	Q9FXE4 arabidopsis
23	359.5	17.8	380	10 Q8RX37	Q8RX37 arabidopsis
24	359.5	17.8	454	4 Q9SD02	Q9SD02 homo sapien
25	358.5	17.5	355	10 Q9S2S3	Q9S2S3 arabidopsis
26	355.5	17.5	355	10 Q81716	Q81716 arabidopsis
27	353.5	17.5	362	10 Q9ZPE9	Q9ZPE9 lotus japon
28	352	17.4	307	10 Q9FCM3	Q9FCM3 arabidopsis
29	352	17.4	392	10 Q9SLA1	Q9SLA1 arabidopsis
30	351	17.4	404	10 Q22200	Q22200 arabidopsis
31	351	17.4	658	10 Q940A2	Q940A2 arabidopsis
32	350	17.3	305	10 Q942N4	Q942N4 oryza sativ
33	350	17.3	357	10 Q9S2S3	Q9S2S3 arabidopsis
34	341.5	16.9	450	11 Q9WVW7	Q9WVW7 rattus norv
35	339	16.8	383	10 Q9LPI2	Q9LPI2 arabidopsis
36	338.5	16.8	396	10 Q9M1P8	Q9M1P8 arabidopsis
37	338.5	16.8	383	10 Q9XEB8	Q9XEB8 arabidopsis
38	338.5	16.8	405	10 Q9LME9	Q9LME9 arabidopsis
39	338	16.7	323	11 Q9EDB2	Q9EDB2 mus musculu
40	338	16.7	326	11 Q9EDB2	Q9EDB2 mus musculu
41	338	16.7	326	11 Q9EDB2	Q9EDB2 mus musculu
42	337.5	16.7	380	10 Q8R4T7	Q8R4T7 mesembryant
43	337.5	16.7	380	10 P93006	P93006 medicago sa
44	336.5	16.7	381	10 Q24078	Q24078 medicago sa
45	336.5	16.7	396	10 Q80871	Q80871 arabidopsis

ALIGNMENTS

RESULT 1
Q9H0C8 PRELIMINARY; PRT: 392 AA.
ID Q9H0C8
AC Q9H0C8
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 42.9 kDa protein (Integrin-linked kinase-associated
DE serine/threonine phosphatase 2C).
CN DKPZP434J2031
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Leung-Hagesteijn C., Mewes H.W., Weil B., Wiemann S.;
RA "Modulation of integrin signal transduction by ILKAP, a protein
RT phosphatase 2C associating with the integrin-linked kinase, ILK1".
RL EMBO J. 0:0-0(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Strassberg R.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL136850; CAB66784.1; -;
DR EMBL: AY024365; AK07736.1; -;
DR EMBL: BC006576; AAH06576.1; -;
DR HSSP: P35813; 1A60.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00352; PP2C; 1.
DR SMART: SM00351; PP2C_Sig; 1.

DR PROSITE: PS01032; PP2C; 1.
KW Hypothetical protein; Kinase.
SQ SEQUENCE 392 AA; 42906 MW; AF6ACC98508CBEA3 CRC64;

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 4,4e-156;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPFDLPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPFDLPASSGDSG 60
QY 61 STATSIQWVKTGKGAOKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 STATSIQWVKTGKGAOKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
QY 121 MODAVHILNDITIEECRPPSSLTTRVSYFAVFDGHGIRASKRAAONLHONLIRKPKGV 180
DB 121 MODAVHILNDITIEECRPPSSLTTRVSYFAVFDGHGIRASKRAAONLHONLIRKPKGV 180
QY 181 ISEVTKVRKCLLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGDSPAI 240
DB 181 ISEVTKVRKCLLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGDSPAI 240
QY 241 LCRVNEESQKHAALSLSKHNPTQYEERMRIQKAGNVBDGVLGVLEYSRSIGDQYKR 300
DB 241 LCRVNEESQKHAALSLSKHNPTQYEERMRIQKAGNVBDGVLGVLEYSRSIGDQYKR 300
QY 301 CGVTSVPDIRCOLPNDPFIILACDGLFKVTPPEAVNFILSCLEDEKIQTRREGKSAAD 360
DB 301 CGVTSVPDIRCOLPNDPFIILACDGLFKVTPPEAVNFILSCLEDEKIQTRREGKSAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
```

RESULT 2

Q8R0F6 PRELIMINARY; PRT; 392 AA.
AC 08R0F6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to protein phosphatase 2C.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026953; AAH26953.1; -
SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DAC987176 CRC64;

Query Match 95.9%; Score 1935; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 2.5e-149;
Matches 373; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPFDLPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPFDLPASSGDSG 60
QY 61 STATSIQWVKTGKGAOKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 STATSIQWVKTGKGAOKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
QY 121 MODAVHILNDITIEECRPPSSLTTRVSYFAVFDGHGIRASKRAAONLHONLIRKPKGV 180
DB 121 MODAVHILNDITIEECRPPSSLTTRVSYFAVFDGHGIRASKRAAONLHONLIRKPKGV 180
```

```
QY 181 ISEVTKVRKCLLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGDSPAI 240
DB 181 ISEVTKVRKCLLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGDSPAI 240
QY 241 LCRVNEESQKHAALSLSKHNPTQYEERMRIQKAGNVBDGVLGVLEYSRSIGDQYKR 300
DB 241 LCRVNEESQKHAALSLSKHNPTQYEERMRIQKAGNVBDGVLGVLEYSRSIGDQYKR 300
QY 301 CGVTSVPDIRCOLPNDPFIILACDGLFKVTPPEAVNFILSCLEDEKIQTRREGKSAAD 360
DB 301 CGVTSVPDIRCOLPNDPFIILACDGLFKVTPPEAVNFILSCLEDEKIQTRREGKPAVD 360
QY 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVWVRIGH 392
```

RESULT 3

Q92126 PRELIMINARY; PRT; 392 AA.
AC Q92126;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Protein phosphatase 2C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99074314; PubMed=9857069;
RA Tong Y., Quirion R., Shen S.H.;
RT "Cloning and characterization of a novel mammalian PP2C isozyme."
RL J. Biol. Chem. 273:35282-35290(1998).
DR EMBL; AF095927; AAC97497.1; -.
DR HSP; P35813; IAOQ.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-STG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 392 AA; 42744 MW; 1468FDE0BA60D915 CRC64;

Query Match 95.7%; Score 1931; DB 11; Length 392;
Best Local Similarity 95.2%; Pred. No. 5.3e-149;
Matches 373; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

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QY 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPFDLPASSGDSG 60
DB 1 MDLFGDLPEPERSPPRAACKEAOKGFLPDDLPASSTDSGSGGFLPFDLPASSGDSG 60
QY 61 STATSIQWVKTGKGAOKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 STATSIQWVKTGKGAOKAKKTSEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
QY 121 MODAVHILNDITIEECRPPSSLTTRVSYFAVFDGHGIRASKRAAONLHONLIRKPKGV 180
DB 121 MODAVHILNDITIEECRPPSSLTTRVSYFAVFDGHGIRASKRAAONLHONLIRKPKGV 180
QY 181 ISEVTKVRKCLLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGDSPAI 240
DB 181 ISEVTKVRKCLLDTEFKHTDEEFLKQASSOKPAWKDSTATCYLAVDNILYIANLGDSPAI 240
QY 241 LCRVNEESQKHAALSLSKHNPTQYEERMRIQKAGNVBDGVLGVLEYSRSIGDQYKR 300
DB 241 LCRVNEESQKHAALSLSKHNPTQYEERMRIQKAGNVBDGVLGVLEYSRSIGDQYKR 300
QY 301 CGVTSVPDIRCOLPNDPFIILACDGLFKVTPPEAVNFILSCLEDEKIQTRREGKSAAD 360
DB 301 CGVTSVPDIRCOLPNDPFIILACDGLFKVTPPEAVNFILSCLEDEKIQTRREGKPAVD 360
```

```
OY 361 ARYEACNRLANKAVORGSDADNTVMYVRIGH 392
DB 361 ARYEACNRLANKAVORGSDADNTVMYVRIGH 392

RESULT 4
OYDC99 PRELIMINARY; PRT; 272 AA.
ID O9DC99;
AC O9DC99;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 0710007A14Rik protein.
GN 0710007A14Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRIN;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boftelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK003007; BAB2508.1; -.
DR HSSP: P35813; IAG0.
DR MGD: MGI:1914694; 0710007A14Rik.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
SQ SEQUENCE 272 AA; 30279 MW; 485F2959D91BA63D CRC64;

Query Match 68.7%; Score 1386; DB 11; Length 272;
Best Local Similarity 97.8%; Pred. No. 7, 3e-105;
Matches 266; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 361 ARYEACNRLANKAVORGSDADNTVMYVRIGH 392
DB 241 ARYEACNRLANKAVORGSDADNTVMYVRIGH 272

RESULT 5
OYCS46 PRELIMINARY; PRT; 212 AA.
ID O9CS46;
AC O9CS46;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 0710007A14Rik protein (Fragment).
GN 0710007A14Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flieschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Oikido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boftelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Guelinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald C., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK019158; BAB31574.1; -.
DR HSSP: P35813; IAG0.
DR MGD: MGI:1914694; 0710007A14Rik.
DR InterPro: IPR001932; PP2C.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR NON_TER 1
FT SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Query Match 53.4%; Score 1078; DB 11; Length 212;
Best Local Similarity 98.1%; Pred. No. 6, 1e-80;
Matches 208; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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0920T2          PRELIMINARY:      PRT:      167 AA.
AC 0920T2:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical 18.8 kDa protein (Fragment).
GN 071007A14RLK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Stohard P.M., Pillgrim D.;
RT "Isolation of PP2C sequences using degenerate-oligo PCR.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF117831; AAD17234.1; -.
DR HSSP: P35813; IAGO.
DR MGD: MGI:1914694; 071007A14RLK.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
KW Hypothetical protein.
FT NON_TER 1
FT TER 167
SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2E9D9DD95B CRC64;

Query Match          42.4%; Score 856; DB 11; Length 167;
Best Local Similarity 98.8%; Pred. No. 5.1e-62;
Matches 165; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 157 IRASFAAQNHLNLRKPKGDVTSVEKTKRCLDTPFKHDEFLKASSOKPAWKDG 216
DB 1 IRASFLAQNHLNLRKPKGDITISVEKTKRCLDTPFKHDEFLKASSOKPAWKDG 60

QY 217 STATCVLANVDNLIYIANLGDRAILCRYNESQKHAALSLSEHNPTQYEEMRIQKAG 276
DB 61 STATCVLANVDNLIYIANLGDRAILCRYNESQKHAALSLSEHNPTQYEEMRIQKAG 120

QY 277 NVRDGRVLCVLEVSIGDGQYKRCGVSVPIRRCQLTPNDRFILL 323
DB 121 NVRDGRVLCVLEVSIGDGQYKRCGVSVPIRRCQLTPNDRFILL 167

RESULT 7
09LMT1          PRELIMINARY:      PRT:      341 AA.
AC 09LMT1:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE T10F20.4 protein.
GN T10F20.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
RA Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
RA Federgrist N.A., Theologis A.;
RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC034107; AAF97840.1; -.
DR HSSP: P35813; IAGO.

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DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C-SIG; 1.
SQ SEQUENCE 341 AA; 37367 MW; 6873C0CEB2310195 CRC64;

Query Match          23.8%; Score 481; DB 10; Length 341;
Best Local Similarity 35.8%; Pred. No. 4.9e-31;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;

QY 78 KRKTSSEKNGSEELY-----EKVKCKASSYI-----FGLKGYVAERKCEEMODAHYI 127
DB 24 KAKKSEEVSGGEAAVAVGNREAEEDKPSFVSEKKEFLVADVADKARHTMEDVWVY 83

QY 128 LNDITEECRPPSSLITRVYFAVFDGGHGRSKFAONLHNLIRKPKGVISVEKTV 187
DB 84 LPDASIDF--PCTL--KCHFAITDHGGRLAEPAKHLHLNVLASAGLPRELDLV-KVA 138

QY 188 KRCLDTPFKHDEEFLKQASOKPAWKDGSTATCVLANVDNLIYIANLGDRAILCR---- 243
DB 139 KKAILEGFRRKTDLLQKSVS--GGWQDGAFAVCWILDQKFFVANIGDAKAVLARSSYT 196

QY 244 -----YNESQKHAALSLSEHNPTQYEEMRIQKAGNV-RDGRVLCVLEVSIGDGQ 297
DB 197 NELGNHTEAGNPLKAIVLREHKAITYPOERSRIQSGGVSSNGRLOGRLVSRAGFGRH 256

QY 298 YKRCGVTSVPDIRRCQLTPNDRFILLACDGLFKVFPPEAVNFIISLCLEDEKIQRECKS 357
DB 257 FKRFVSAITPDTHAFELTERENFMILGCDLMEVGPSPDAVGFVKLL-----KEG-- 307

QY 358 AADARYEAACNLANKAV-QRCGADNVTVWVY 388
DB 308 ---LHVSTVSRLVKEAVKERRCKDNCATVIV 336

RESULT 8
0944K0          PRELIMINARY:      PRT:      351 AA.
AC 0944K0:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE At1g18030/T10F20_3.
GN At1g18030.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF428352; AAL16282.1; -.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C; 1.
SQ SEQUENCE 351 AA; 38514 MW; AFE224E0EE003229 CRC64;

Query Match          23.8%; Score 480; DB 10; Length 351;
Best Local Similarity 35.8%; Pred. No. 6.1e-31;
Matches 119; Conservative 66; Mismatches 107; Indels 40; Gaps 11;

QY 78 KRKTSSEKNGSEELY-----EKVKCKASSYI-----FGLKGYVAERKCEEMODAHYI 127
DB 34 KAKKSEEVSGGEAAVAVGNREAEEDKPSFVSEKKEFLVADVADKARHTMEDVWVY 93

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01-JUN-2002 (TREMblrel. 21, Created)
01-JUN-2002 (TREMblrel. 21, Last sequence update)
01-JUN-2002 (TREMblrel. 21, Last annotation update)
Hypothetical 33.2 kDa protein.
GN AY631750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702.
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.,
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY080658; AAL86334.1; -.
KW Hypothetical protein.
SQ SEQUENCE 311 AA; 33247 MW; SE3098E91F116BFD CRC64;
Query Match 19.7%; Score 398.5; DB 10; Length 311;
Best Local Similarity 39.3%; Pred. No. 2,2e-24;
Matches 112; Conservative 40; Mismatches 88; Indels 45; Gaps 12;
QY 109 GYVARKGEREMODAHVILNDITEECRPSSLITRVSYFAVFDGHCGRASKFAAQLH 168
ID 0883P1 PRELIMINARY; PRT; 243 AA.
AC 0883P1;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 26.7 kDa protein.
GN 24K23.16.
OS Oryza sativa (Japanica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=35947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV_NIPPONBARE;
RA Park Y.-J., Roslows N., Ramakrishna W., Sanmiquel P., Shiof B.,
RA Ma J., Jiang Z., Kleinof A., Bennetzen J.,
RT "Sequence characterization of orthologous regions in the barley and
RL rice genomes."
EMBL: AF490497; AAL87187.1; -.

Hypothetical protein.
SQ SEQUENCE 243 AA; 26734 MW; 8B481E17F559CE5F CRC64;
Query Match 18.9%; Score 381.5; DB 10; Length 243;
Best Local Similarity 37.9%; Pred. No. 3.8e-23;
Matches 96; Conservative 43; Mismatches 75; Indels 39; Gaps 7;
QY 145 VSYFAVFDGHCGRASKFAAQLHONLIR--KFKGDIYSEKVRKCLDTPFKHTDEEF 202
ID 0883P1 PRELIMINARY; PRT; 420 AA.
AC 0883P1;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.,
RT "Arabidopsis cDNA clones."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY065026; AAL57666.1; -.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C-like.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00332; PP2C_1.
DR SMART: SM00331; PP2C-STG; 1.
DR PROSITE: PS01032; PP2C; UNKNOWN_1.
SQ SEQUENCE 420 AA; 45752 MW; 2DF6960D75BF9058 CRC64;
Query Match 18.3%; Score 368.5; DB 10; Length 420;
Best Local Similarity 32.8%; Pred. No. 9.5e-22;
Matches 112; Conservative 60; Mismatches 108; Indels 61; Gaps 13;
QY 64 TSISQWKTTEGKARKTSEEKNGSEELVEKKVCKASSVIFGLK-----GYVARK 115
ID 0883P1 PRELIMINARY; PRT; 243 AA.
AC 0883P1;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 26.7 kDa protein.
GN 24K23.16.
OS Oryza sativa (Japanica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=35947;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV_NIPPONBARE;
RA Park Y.-J., Roslows N., Ramakrishna W., Sanmiquel P., Shiof B.,
RA Ma J., Jiang Z., Kleinof A., Bennetzen J.,
RT "Sequence characterization of orthologous regions in the barley and
RL rice genomes."
EMBL: AF490497; AAL87187.1; -.

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QY 176 PKGDVISEVETKRCCLDPTFKHTDEFLKQASOKPAMK-DGSTATCVLAVNLIYANL 234
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 160 PQ-----FLDTFKLALNETYKQDVALE---SEKQTYRNDOSRTASAAVLGNHLYAVN 211
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 235 GSRALICRYNEESOKHAALSLSKEHNPTQYERMRIOKAGNVR---DGRVIGYEVSR 291
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 212 GDSRTIV-----SKAGALALSDHRCFNRSDERKRKIESAGSVIMAGTMRVGGVLMASR 265
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 292 SIGDQYKRCGYTSVPDIRRCQLTPNDRIPLACDGLFKVFTPEEAVNFILSCLEDKIQ 351
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 266 ALGNRLMKQF-VVAEPEIODEIDHEAELLIVLASDGLMVDVFNEDAV--ALAOSEEP-- 320
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 352 TREGKSADARYEAACNRLANKAVORGSGADNVTYVVRIGH 392
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 321 -----EAAARKLTDTAFSRGSAADNITCIYVFRH 349
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 14
ID 081773 PRELIMINARY; PRT; 389 AA.
AC 081773;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical 42.6 kDa protein.
GN F28M20.60 OR AT4G31750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Hohelsel J.,
RA Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.;
RN Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031004; CA19748.1; -.
DR EMBL; AL161579; CAB79893.1; -.
DR HSSP; P35813; 1A60.
DR InterPro; IPR001933; Mitoch_carrier.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C.1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOMN_1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein
SQ SEQUENCE 389 AA; 42562 MW; A7GC39764ECLDEA CRC64;

Query Match 18.2%; Score 368; DB 10; Length 389;
Best Local Similarity 33.7%; Pred. No. 9, 3e-22;
Matches 114; Conservative 40; Mismatches 86; Indels 98; Gaps 14;

QY 109 GYAERKGEREMODAHVILNDITECRPPSLITRYSYFAVFDHGGRIRASKPAQNLH 168
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 60 GY-ASSPGKRSMDEFEYTRIDVEG-----ELVGLFGVFDHGGRARAAYVQNLF 110
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 169 QNLIRKPKGDVISEVETKRCCLDPTFKHTDEFLKQASOKPAMK-DGSTATCVLAVN 227
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 111 SNLR-HPK--FIS---DTTAIDADAYNODSEFLKSENSQ---RAGSTASTAIIYGD 161
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 228 ILYIANIGDSRALICRYNEESOKHAALSLSKEHNPTQYERMRIOKAGNVR---DGRVL 284
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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DQ 162 RLVAANODDERAVYICGN-----AIAVSDHPRPDSDERQRIEDAGGFVMAQTYRWG 215
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 285 GYLVESISIDQYKRCGYTSVPDIR-----PRTPEEAVNFILSCLEDKIQ 310
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 216 GYLAVSRFGRLIKQF-VVADEIQLVTFQONLLIKATLLTIENLHWISYSL 274
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 311 -----RCQLTPNDR-----FILACDGLFKVFTPEEAVNFILSCLEDKIQ 351
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 275 NGLTQNLFRSLISINSKFOEEKVDSLEFLILASDGLMDVDSNEEAVGMI-KAIDP-- 330
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 352 TREGKSADARYEAACNRLANKAVORGSGADNVTYVVRIGH 389
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 331 -----EGCAKRLMEAYORGSGADNITCVVR 356
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

RESULT 15
ID 015743 PRELIMINARY; PRT; 975 AA.
AC 015743;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Spalten.
GN SPAN.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium.
OX NCBI_TaxId=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-A93
RC MEDLINE=98252837; PubMed=9585512;
RX Audry L., Firtel R.A.;
RA Spalten, a protein containing Galpha-protein-like and PP2C domains,
RT is essential for cell-type differentiation in Dictyostellium.";
RL Genes Dev. 12:1525-1538(1998).
DR EMBL; AF019985; AAB70844.1; -.
DR HSSP; P35813; 1A60.
DR InterPro; IPR001019; Gprotelin_alpha.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001933; PP2C-like.
DR Pfam; PF00503; G-alpha; 1.
DR Pfam; PF00481; PP2C; 1.
DR Prodom; PD000281; Gprotelin_alpha; 1.
DR SMART; SM00275; G-alpha; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 975 AA; 109016 MW; BB8322F5026D24F CRC64;

Query Match 18.2%; Score 368; DB 5; Length 975;
Best Local Similarity 29.1%; Pred. No. 3, 5e-21;
Matches 118; Conservative 56; Mismatches 152; Indels 80; Gaps 17;

QY 8 PEPEPSPPRAAGKEAQKGLPDDLPASSSTDSSGGPLFLPDLPRASSGDSGLATYSIS 67
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 620 KPFKEKRPFI--KEPKKEPVK--ESKPKKE-----PRTPEEKEKPEP 661
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 68 QMVTGKGAARKTS-----EEKNGSEEL---VEKKYCKASSVIFGLKTYAERKE 117
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 662 KPEKRTKPEKRTKSYVDGAASKKNAGDSGNGSGVSKTKLSG--FG-----SLQGR 713
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 118 REEMODAHVILNDITECR---PPSSLITRYSYFAVFDHGGRIRASKPAQNLH 172
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 714 RKNMEDHVLINLMGAAYVYNGPPKDI--PISYAAVYDGHGRTSTLLPTLVNHCIVNS 771
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 173 KRFKPGDVISEVETKRCCLDPTFKHTDEFLKQASOKPAMKDGSTATCVLAVNLIYIA 232
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 772 QSFRCG-----YDQAFRDYVABADDIVIEKE-----KSGSYGVALLVGNKLYTA 818
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 233 NLGDSRALICRYNEESOKHAALS-----LSKEHNPTQYERMRIOKAGNVRDGVLCVL 287
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
DQ 819 NVGSEIYLARAQPNANPKNPGVTPYEPVLLSYKHLASDDQKKRKYVTDGLGMIIFNRLFGSL 878
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

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QY 288 EVSRSIGDGYKR-----CGVTSPDIRRCOLTPNDREILACDGLFKVFTPEEAVNFIL 342
| | | | | : | | | | | : | | | | | : | | | | | :
Db 879 AVSRSEFGDKYKKEGKKFC--VSDPYQTDTDLTARDHFFILACDGLMDKVEYDEAVQEV- 935
QY 343 SCLDEKIQTRBCKSAADARIEACNRLANKAVORGADNVTVMVY 388
: : | | | : | | | : | | | : | | | : | | | :
Db 936 -----QRNIRKIGKSATE-----ISELLAODSDYDRSGSDNITVLVY 970

Search completed: January 17, 2003, 17:44:56
Job time : 39 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:46 ; Search time 39 Seconds

(Without alignments)
1339.340 Million cell updates/sec

Title: US-09-935-124a-2

Perfect score: 2018

Sequence: 1 MDLFGDLPFEPSPRPAAGK.....KAVQSGADNVTVMVVRIGH 392

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	22	AA828791 Human signal trans
2	2018	100.0	392	23	AB805726 Human protein phos
3	2018	100.0	421	22	ABH12317 Human polypeptide
4	2018	100.0	421	22	AA440555 Novel human enzyme
5	2018	100.0	441	22	AAU23566 Novel human enzyme
6	2018	100.0	446	22	AAU22933 Human polypeptide
7	2015	99.9	392	22	AA892585 Human polypeptide
8	2014	99.8	392	22	AA838769 Human polypeptide
9	1457.5	72.2	378	22	ABG09337 Novel human diagno
10	928	46.0	221	22	ABG09336 Novel human diagno

11	533.5	26.4	211	22	ABG07619 Novel human diagno
12	447.5	22.2	138	22	AA023222 Novel human enzyme
13	431.5	21.4	295	21	AA618058 Arabidopsis thalia
14	431.5	21.4	305	21	AA618057 Arabidopsis thalia
15	404	20.0	86	21	AA630424 Human secreted pro
16	391.5	19.4	219	21	AA618059 Arabidopsis thalia
17	370.5	18.4	353	23	AB877579 Physcomitrella pat
18	370.5	18.4	354	21	AA606997 Arabidopsis thalia
19	366.5	18.2	360	21	AA618039 Arabidopsis thalia
20	366.5	18.2	383	21	AA618039 Arabidopsis thalia
21	366.5	18.2	420	21	AA639774 Arabidopsis thalia
22	366.5	18.2	454	23	AB808388 Human-derived prot
23	364	18.0	358	21	AA618041 Arabidopsis thalia
24	364	18.0	358	21	AA639776 Arabidopsis thalia
25	364	18.0	359	21	AA618040 Arabidopsis thalia
26	364	18.0	359	21	AA639775 Arabidopsis thalia
27	363	18.0	309	21	AA606998 Arabidopsis thalia
28	358.5	17.8	361	23	AB892620 Herbicidially activ
29	353.5	17.5	355	21	AA643887 Trichoderma reesei
30	353.5	17.5	438	22	AA62980 Arabidopsis thalia
31	353.5	17.5	438	22	AA615376 Arabidopsis thalia
32	352.5	17.5	434	22	AA601344 Arabidopsis thalia
33	352	17.4	276	21	AA616903 Arabidopsis thalia
34	350	17.3	357	21	AA643237 Arabidopsis thalia
35	349	17.3	329	21	AA643228 Arabidopsis thalia
36	349	17.1	327	21	AA643868 Arabidopsis thalia
37	345.5	16.9	434	22	AA601346 Arabidopsis thalia
38	341.5	16.9	236	21	AA616904 Arabidopsis thalia
39	341	16.9	322	21	AA643229 Arabidopsis thalia
40	339	16.8	320	21	AA643889 Arabidopsis thalia
41	338.5	16.8	383	21	AA609824 Arabidopsis thalia
42	338	16.8	382	23	AB857083 Mouse ischaemic co
43	337.5	16.7	360	21	AA677093 A. thaliana enviro
44	336	16.7	387	22	AB862019 Drosophila melanog
45	336	16.7	382	23	AB61491 Human NF-kB activa

ALIGNMENTS

RESULT 1	AA828791 standard; Protein; 392 AA.
ID	AA828791
XX	AA828791;
AC	13-FEB-2001 (first entry)
XX	
DT	Human hydroxylase-like molecule 2 protein.
XX	
DE	Hydroxylase-like molecule; human; cell proliferation disorder.
KW	autoimmune; cancer; AIDS; acquired immune deficiency syndrome.
XX	
OS	Homo sapiens.
XX	
PN	US6132964-A.
XX	
PD	17-OCT-2000.
XX	
PF	06-FEB-1998; 98US-0013881.
XX	
PR	06-FEB-1998; 98US-0013881.
XX	
PA	(INCYTE) INCYTE PHARM INC.
XX	
PI	Bandman O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;
XX	WPI; 2001-006133/01.
DR	N-PSDB; AAC60224.
XX	
PT	New human hydroxylase-like molecules (HHLMs) and polynucleotides encoding
PT	the HHLMs, useful for diagnosing, treating or preventing cell
PT	proliferation (e.g. bone cancer) or autoimmune disorders(e.g. AIDS or

PT asthma) -
XX
PS Claim 1; Column 43-46; 38pp; English.
XX
CC The present invention relates to isolated and purified cDNA encoding a
CC human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The
CC HHLM DNAs and polypeptides are useful for diagnosing, treating or
CC preventing cell proliferation disorders and autoimmune disorders. Cell
CC proliferation disorders include cancers, autoimmune disorders include
CC AIDS (acquired immune deficiency syndrome). The present sequence
CC is a HHLM protein of the invention.
XX
SQ Sequence 392 AA;
Query Match 100.0%; Score 2018; DB 22; Length 392;
Best Local Similarity 100.0%; Pred. No. 5,7e-187;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPAPGAKGKQKPLFDLLPPASSTDSGGGGLFDDLLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPAPGAKGKQKPLFDLLPPASSTDSGGGGLFDDLLPPASSGDSG 60
QY 61 SLATSIQMVKTEGKAGKRTSEEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 SLATSIQMVKTEGKAGKRTSEEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
QY 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
DB 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
QY 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGTATCVLAVDNLITYANLGDSPAI 240
DB 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGTATCVLAVDNLITYANLGDSPAI 240
QY 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLVSVSIGDGQYKR 300
DB 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLVSVSIGDGQYKR 300
QY 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
DB 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
RESULT 2
ABB05726
ID ABB05726 standard; Protein; 392 AA.
XX
AC ABB05726;
XX
DT 30-APR-2002 (first entry)
XX
DE Human signal transduction protein clone tes3_31j20.
XX
KW Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200198454-A2.
XX
PD 27-DEC-2001.
XX
PF 25-APR-2001; 2001MO-IB02050.
XX
PR 25-APR-2000; 2000US-199380P.
XX
PA (GEHU) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S; ◀

XX
DR WPI; 2002-055860/07.
DR N-PSDB; ABA93763.
XX
PT Human cDNA sequences and clones derived from human fetal brain, fetal
PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
PT screening and therapy -
XX
PS Claim 1; Page 377; 61pp; English.
XX
CC The present invention describes assemblies and computer readable media
CC comprising novel human cDNA sequences and clones derived from human
CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
CC present invention which encode the proteins given in ABB05662 to
CC ABB05729. The human cDNA sequences and clones can be used in gene
CC therapy. The clones may be used in profiling assays, for providing large arrays
CC of human genetic material for implementing large-scale screening
CC strategies and for treating diseases via gene therapy procedures.
XX
SQ Sequence 392 AA;
Query Match 100.0%; Score 2018; DB 23; Length 392;
Best Local Similarity 100.0%; Pred. No. 5,7e-187;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPAPGAKGKQKPLFDLLPPASSTDSGGGGLFDDLLPPASSGDSG 60
DB 1 MDLFGDLPEPERSPPAPGAKGKQKPLFDLLPPASSTDSGGGGLFDDLLPPASSGDSG 60
QY 61 SLATSIQMVKTEGKAGKRTSEEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
DB 61 SLATSIQMVKTEGKAGKRTSEEEKNGSEELVEKKVCASSVIFGLKGYAERKGEREE 120
QY 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
DB 121 MODAHVILNDITEBCRPSSLITRVSYFAVFDGHCIRASKFAAQNHLIRKPKGDV 180
QY 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGTATCVLAVDNLITYANLGDSPAI 240
DB 181 ISVEKTVKRCLLDFPKHTDEEFLKQASSQKPAWKDGTATCVLAVDNLITYANLGDSPAI 240
QY 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLVSVSIGDGQYKR 300
DB 241 LCARYNEESQKHAALSLSKENHPTQYEERMRIQKAGNRRDGRVLGVLVSVSIGDGQYKR 300
QY 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
DB 301 CGVTSVPDIRRCQLTLPNDRFTLLACDGLFKVFTPEEAVNFTLSCLEDEKIQTRREGSKAAD 360
QY 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
DB 361 ARYEACNRLANKAVQSGADNVTVVVRIGH 392
RESULT 3
ABB12317
ID ABB12317 standard; peptide; 421 AA.
XX
AC ABB12317;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human protein phosphatase 2C homologue, SEQ ID NO:2687.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;

PR 25-SEP-2000: 2000US-02344998.
PR 26-SEP-2000: 2000US-0235484.
PR 27-SEP-2000: 2000US-0235834.
PR 27-SEP-2000: 2000US-0235834.
PR 29-SEP-2000: 2000US-0236327.
PR 29-SEP-2000: 2000US-0236327.
PR 29-SEP-2000: 2000US-0236359.
PR 29-SEP-2000: 2000US-0236359.
PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 13-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
PR 20-OCT-2000: 2000US-0241221.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241786.
PR 20-OCT-2000: 2000US-0241787.
PR 20-OCT-2000: 2000US-0241808.
PR 20-OCT-2000: 2000US-0241809.
PR 01-NOV-2000: 2000US-0241826.
PR 01-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0246474.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
PR 08-NOV-2000: 2000US-0246477.
PR 08-NOV-2000: 2000US-0246478.
PR 08-NOV-2000: 2000US-0246523.
PR 08-NOV-2000: 2000US-0246524.
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PR 08-NOV-2000: 2000US-0246610.
PR 08-NOV-2000: 2000US-0246611.
PR 08-NOV-2000: 2000US-0246613.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
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PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249224.
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PR 17-NOV-2000: 2000US-0249225.
PR 17-NOV-2000: 2000US-0249225.
PR 17-NOV-2000: 2000US-0249229.
PR 01-DEC-2000: 2000US-0249300.
PR 01-DEC-2000: 2000US-0250160.
PR 01-DEC-2000: 2000US-0250391.
PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0256719.
PR 06-DEC-2000: 2000US-0251479.
PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251989.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barrash SC, Ruben SM;
XX WPI: 2001-465566/50.
XX N-PSDB: AAS41436.
DR
XX Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases
XX
PS Claim 11: SEQ ID NO.1562; 1180pp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AA540785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma) cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AA022915-AA023814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
CC
CC Sequence 441 AA:
SQ
Query Match 100.0%; Score 2018; DB 22; Length 441;
Best Local Similarity 100.0%; Pred. No. 6.9e-187;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLFGDLPEPERSPPAPKAEAKGGLPDDLPASSSTDSGGLPFDLPASSGDSG 60
DB 50 MDLFGDLPEPERSPPAPKAEAKGGLPDDLPASSSTDSGGLPFDLPASSGDSG 109
QY 61 SLATISQWVTEKGAKKRTSEEEKNGSEELVEKKYCKKASSYFGLKGVAERGEREE 120
DB 110 SLATISQWVTEKGAKKRTSEEEKNGSEELVEKKYCKKASSYFGLKGVAERGEREE 169
QY 121 MODAVIILNDITTECPRPSSLTIRVSYFAPVPGHGRASPAONLHMLRKPCKDY 180
DB 170 MODAVIILNDITTECPRPSSLTIRVSYFAPVPGHGRASPAONLHMLRKPCKDY 229
QY 181 ISEVTVKRCLLDTFKHTDEEFLKQASSQPKMKDGSATCVLAVNDILYIANLGDSRAI 240
DB 230 ISEVTVKRCLLDTFKHTDEEFLKQASSQPKMKDGSATCVLAVNDILYIANLGDSRAI 289
QY 241 ICRVNEESQKHAALSLSKEHNPTQYERMRIOKAGNVRGRLVGLVSRISGQYKR 300
DB 290 ICRVNEESQKHAALSLSKEHNPTQYERMRIOKAGNVRGRLVGLVSRISGQYKR 349
QY 301 CGVTSVPDIRCQLTPMDRFLIACDGLFKYFTEPEAVNFIISCLDEKIQTRREGKSAD 360
DB 350 CGVTSVPDIRCQLTPMDRFLIACDGLFKYFTEPEAVNFIISCLDEKIQTRREGKSAD 409
QY 361 ARYEACNRLANKAVQSGSADNVTWVVRIGH 392
DB 410 ARYEACNRLANKAVQSGSADNVTWVVRIGH 441
RESULT 6
AAU22933
ID AAU22933 standard; Protein: 446 AA.

XX	AAU22933;		PR	12-SEP-2000;	2000US-0231968.
AC			PR	14-SEP-2000;	2000US-0232397.
XX			PR	14-SEP-2000;	2000US-0232398.
DT	17-DEC-2001 (first entry)		PR	14-SEP-2000;	2000US-0232399.
XX			PR	14-SEP-2000;	2000US-0232400.
DE	Novel human enzyme polypeptide #19.		PR	14-SEP-2000;	2000US-0232401.
XX			PR	14-SEP-2000;	2000US-0233063.
KW	Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;		PR	14-SEP-2000;	2000US-0233064.
KW	lyase; hyperproliferative disorder; immunodeficiency disorder;		PR	14-SEP-2000;	2000US-0233065.
KW	autoimmune disorder; neurological disorder; metabolic disorder;		PR	21-SEP-2000;	2000US-0234223.
KW	inflammatory disorder; cardiovascular disorder; reproductive disorder;		PR	21-SEP-2000;	2000US-0234274.
KW	blood-related disorder; infectious disorder; cytostatic; anti arthritic;		PR	25-SEP-2000;	2000US-0234997.
KW	nephrotropic; anticoagulant.		PR	25-SEP-2000;	2000US-0234998.
XX			PR	26-SEP-2000;	2000US-0235484.
OS	Homo sapiens.		PR	27-SEP-2000;	2000US-0235834.
XX			PR	27-SEP-2000;	2000US-0235836.
PN	WO200155301-A2.		PR	29-SEP-2000;	2000US-0236327.
XX			PR	29-SEP-2000;	2000US-0236327.
PD	02-AUG-2001.		PR	29-SEP-2000;	2000US-0236367.
XX			PR	29-SEP-2000;	2000US-0236368.
XX			PR	29-SEP-2000;	2000US-0236369.
PF	17-JAN-2001; 2001WO-US01239.		PR	02-OCT-2000;	2000US-0236802.
XX			PR	02-OCT-2000;	2000US-0237037.
PR	31-JAN-2000; 2000US-0179065.		PR	02-OCT-2000;	2000US-0237038.
PR	04-FEB-2000; 2000US-0180628.		PR	02-OCT-2000;	2000US-0237039.
PR	24-FEB-2000; 2000US-0184664.		PR	13-OCT-2000;	2000US-0239335.
PR	02-MAR-2000; 2000US-0186350.		PR	13-OCT-2000;	2000US-0239337.
PR	16-MAR-2000; 2000US-0189874.		PR	20-OCT-2000;	2000US-0240960.
PR	17-MAR-2000; 2000US-0190076.		PR	20-OCT-2000;	2000US-0241221.
PR	18-APR-2000; 2000US-0198123.		PR	20-OCT-2000;	2000US-0241221.
PR	19-MAY-2000; 2000US-0205515.		PR	20-OCT-2000;	2000US-0241785.
PR	07-JUN-2000; 2000US-0209467.		PR	20-OCT-2000;	2000US-0241786.
PR	28-JUN-2000; 2000US-0214886.		PR	20-OCT-2000;	2000US-0241787.
PR	30-JUN-2000; 2000US-0215135.		PR	20-OCT-2000;	2000US-0241808.
PR	07-JUL-2000; 2000US-0216647.		PR	20-OCT-2000;	2000US-0241809.
PR	07-JUL-2000; 2000US-0216880.		PR	20-OCT-2000;	2000US-0241826.
PR	11-JUL-2000; 2000US-0217487.		PR	01-NOV-2000;	2000US-0244617.
PR	11-JUL-2000; 2000US-0217496.		PR	08-NOV-2000;	2000US-0246475.
PR	14-JUL-2000; 2000US-0218290.		PR	08-NOV-2000;	2000US-0246476.
PR	26-JUL-2000; 2000US-0220963.		PR	08-NOV-2000;	2000US-0246525.
PR	26-JUL-2000; 2000US-0220964.		PR	08-NOV-2000;	2000US-0246526.
PR	14-AUG-2000; 2000US-0224518.		PR	08-NOV-2000;	2000US-0246527.
PR	14-AUG-2000; 2000US-0224519.		PR	08-NOV-2000;	2000US-0246528.
PR	14-AUG-2000; 2000US-0225213.		PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000; 2000US-0225214.		PR	08-NOV-2000;	2000US-0246532.
PR	14-AUG-2000; 2000US-0225266.		PR	08-NOV-2000;	2000US-0246610.
PR	14-AUG-2000; 2000US-0225267.		PR	08-NOV-2000;	2000US-0246611.
PR	14-AUG-2000; 2000US-0225268.		PR	08-NOV-2000;	2000US-0246613.
PR	14-AUG-2000; 2000US-0225270.		PR	17-NOV-2000;	2000US-0249207.
PR	14-AUG-2000; 2000US-0225447.		PR	17-NOV-2000;	2000US-0249208.
PR	14-AUG-2000; 2000US-0225757.		PR	17-NOV-2000;	2000US-0249209.
PR	14-AUG-2000; 2000US-0225758.		PR	17-NOV-2000;	2000US-0249210.
PR	14-AUG-2000; 2000US-0225759.		PR	17-NOV-2000;	2000US-0249211.
PR	18-AUG-2000; 2000US-0226279.		PR	17-NOV-2000;	2000US-0249212.
PR	22-AUG-2000; 2000US-0226681.		PR	17-NOV-2000;	2000US-0249213.
PR	22-AUG-2000; 2000US-0226868.		PR	17-NOV-2000;	2000US-0249214.
PR	22-AUG-2000; 2000US-0227182.		PR	17-NOV-2000;	2000US-0249215.
PR	23-AUG-2000; 2000US-0227009.		PR	17-NOV-2000;	2000US-0249216.
PR	30-AUG-2000; 2000US-0228924.		PR	17-NOV-2000;	2000US-0249217.
PR	01-SEP-2000; 2000US-0229287.		PR	17-NOV-2000;	2000US-0249218.
PR	01-SEP-2000; 2000US-0229343.		PR	17-NOV-2000;	2000US-0249219.
PR	01-SEP-2000; 2000US-0229344.		PR	17-NOV-2000;	2000US-0249220.
PR	01-SEP-2000; 2000US-0229345.		PR	17-NOV-2000;	2000US-0249221.
PR	05-SEP-2000; 2000US-0229509.		PR	17-NOV-2000;	2000US-0249222.
PR	05-SEP-2000; 2000US-0229513.		PR	17-NOV-2000;	2000US-0249223.
PR	06-SEP-2000; 2000US-0230437.		PR	17-NOV-2000;	2000US-0249224.
PR	06-SEP-2000; 2000US-0230438.		PR	17-NOV-2000;	2000US-0249245.
PR	08-SEP-2000; 2000US-0231242.		PR	17-NOV-2000;	2000US-0249246.
PR	08-SEP-2000; 2000US-0231243.		PR	17-NOV-2000;	2000US-0249247.
PR	08-SEP-2000; 2000US-0231244.		PR	17-NOV-2000;	2000US-0249255.
PR	08-SEP-2000; 2000US-0231413.		PR	17-NOV-2000;	2000US-0249257.
PR	08-SEP-2000; 2000US-0231414.		PR	17-NOV-2000;	2000US-0249299.
PR	08-SEP-2000; 2000US-0232080.		PR	17-NOV-2000;	2000US-0249300.
PR	08-SEP-2000; 2000US-0232081.		PR	01-DEC-2000;	2000US-0250160.

Query Match	99.9%	Score 2015;	DB 22;	Length 392;
Best Local Similarity	99.7%	Pred. NO. 1.1e-186;		
Matches 391; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MDGCDLPEPERSRPPAAGKEAKGCLLPDLPASSDSGSGCLLPDLPASSDSG	60
Dd	1	MDLEGDLPEPERSRPPAAGKEAKGCLLPDLPASSDSGSGCLLPDLPASSDSG	60
QY	61	SLATSISOMVYKTECKGAKRKRTSEEEKNGSEBELYEKKACASVYFGJLKGVAERKGEREE	120
Dd	61	SLATSISOMVYKTECKGAKRKRTSEEEKNGSEBELYEKKACASVYFGJLKGVAERKGEREE	120
QY	121	MODAHVILNDITTECCRPSSCLTRVSYFAVPDGHGGRASKFAAQNHLQNLIRKPKGDV	180
Dd	121	MODAHVILNDITTECCRPSSCLTRVSYFAVPDGHGGRASKFAAQNHLQNLIRKPKGDV	180
QY	181	ISVEKTYKRCCLDFFKHTDEBELKQASOSKPAKMDGSTATCYLAVNDIITIANLGSRAI	240
Dd	181	ISVEKTYKRCCLDFFKHTDEBELKQASOSKPAKMDGSTATCYLAVNDIITIANLGSRAI	240
QY	241	LCRAREESOKHAALSLSEKHEHPITOYEERMRITOKAGAVNRDGRVLGYLEVRSRISGDDQYKR	300
Dd	241	LCRAREESOKHAALSLSEKHEHPITOYEERMRITOKAGAVNRDGRVLGYLEVRSRISGDDQYKR	300
QY	301	CGVTSVPDIRRCOLTPVDRPFIILACDGLFKVFTTPEEAVNFIILSCLDEDEKIQOTREKSSAAD	360
Dd	301	CGVTSVPDIRRCOLTPVDRPFIILACDGLFKVFTTPEEAVNFIILSCLDEDEKIQOTREKSSAAD	360
QY	361	ARYEACNRLANKAVORGSAADNVTVMVVRIGH	392
Dd	361	ARYEACNRLANKAVORGSAADNVTVMVVRIGH	392

RESULT 8
AAM38769
ID AAM38769 standard; Protein; 392 AA

AC	AAM38769;
XX	
DT	22-OCT-2001 (first entry)
XX	

DE Human polypeptide SEQ ID NO 1914.
XX
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

OS	Homo sapiens.
XX	
PN	W0200153312-A1.
WU	

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR	21-JAN-2000;	2000US-0488725
PR	25-APR-2000;	2000US-0552317
PR	09-JUL-2000;	2000US-0598042
PR	19-JUL-2000;	2000US-0620312
PR	03-AUG-2000;	2000US-0653450
PR	14-SEP-2000;	2000US-0662191
PR	19-OCT-2000;	2000US-0690336
PR	23-NOV-2000;	2000US-0721344

PA (HYSE-) HYSEQ INC.

PI	Tang XT,	Liu C,	Asundi V,	Chen R,	Ma Y,	Qian XB,	Ren F,	wang D;
PI	Wang J,	Wang Z,	Wehrman T,	Xu C,	Xue AJ,	Yang Y,	Zhang J;	
PI	zhao Qa,	zhou P,	Goodrich R,	Drmanac RT;				

XX	WPI: 2001-442253/47.
DR	N-PSDB; AA157925.
XX	
PT	Novel nucleic acids and polypeptides, useful for treating disorders
PT	such as central nervous system injuries -
XX	
PS	Example 3; SEQ ID NO 1914; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotid
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Prager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

Sequence 392 AA;

Query Match	99.8%	Score 2014;	DB 22;	Length 392;
Best Local Similarity	99.7%	Pred. No. 1.4e-186;		
Matches 391; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	MDGDLPEBERSRPAKGEAKGILLPDLPASSDSGSGPLLPDLPASSDSG	60
Db	1	MDLEGDLPPEBRSPAPAKGEAKGILLFPDLPASSDSGSGPLLPDLPASSDSG	60
QY	61	SLATSISOMWTEBKGAARKTSEEEKNGSEELVEKKCKAKASVYFGLGKVAERKGEREE	120
Db	61	SLATSISOMWTEBKGAARKTSEEEKNGSEELVEKKCKAKASVYFGLGKVAERKGEREE	120
QY	121	MODAHVTLNDITECRRPSSLITRVSYFAVFDGHGIRASKFAAQNLOHNLIRKFPKGDV	180
Db	121	MODAHVTLNDITECRRPSSLITRVSYFAVFDGHGIRASKFAAQNLOHNLIRKFPKGDV	180
QY	181	ISVEKTVKRCLLDPEFKHTDEEPLKQASQSPAMWDSGTATCVLAVNDILITANIGDSRAI	240
Db	181	ISVEKTVKRCLLDPEFKHTDEEPLKQASQSPAMWDSGTATCVLAVNDILITANIGDSRAI	240
QY	241	LCARYNESSQKHAALSLSKEHNPTQYEEBMRIOKAGCNVROGRVLGYLEVRSITGDGYKR	300
Db	241	LCARYNESSQKHAALSLSKEHNPTQYEEBMRIOKAGCNVROGRVLGYLEVRSITGDGYKR	300
QY	301	CGYTSVPDITRRCOLTPMDRFTLLACDGLFVFTPEEAVNFTLSCLEDEKIQTPREGKSAAD	360
Db	301	CGYTSVPDITRRCOLTPMDRFTLLACDGLFVFTPEEAVNFTLSCLEDEKIQTPREGKSAAD	360
QY	361	ARYEACNRLANKAVOGSADNTVMVVRIGH	392
Db	361	ARYEACNRLANKAVOGSADNTVMVVRIGH	392

RESULT 9
ABG09937
ID ABG09937 standard; Protein; 378 AA

AC ABG09937;

DT 13-FEB-2002 (first entry)

Novel human diagnostic protein #9928.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB: AAS74124.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity
XX PS Claim 20; SEQ ID No 40296; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 378 AA:
Query Match 72.2%. Score 1457.5; DB 22; Length 378;
Best Local Similarity 77.98; Pred. NO. 1.3e-132;
Matches 303; Conservative 13; Mismatches 46; Indels 27; Gaps 6;
OY 20 KEAOKGFLFDLPPASSTDSGGGFLFDLPPASSGDSGSLATSIOMWTEGKAKR 79
DB 1 KEAOKGFLFDLPPASSTDSG-----VVALGTPSPVTLMTLQTRRSKIWRN 49
OY 80 KTSSEKNGSEELVEKKVCK-----ASSVIFGLKGYAERKGEEREMQDAHVI 127
DB 50 SLDYQSKVGAEPWCHERQOKADRFGLGKRGKRVAPSSVIFGLKGYAERKGEEREMQDAHVI 109
OY 128 LNDITECRPPSSLITRVSYFAVFDGAGIRASKFAAOMLHONLRKPKKDVISVEKTV 187
DB 110 LNDITECRPPSSLITRVSYFAVFDGAGIRASKFAAOMLHONLRKPKKDVISVEKTV 169
OY 188 KRCLDTEFKHTDEEFLKQASSOKPAMKDGSTATCVLAVONITLYINLMDSSRAILCRNEE 247
DB 170 KRCLDTEFKHTDEEFLKQASSOKPAMKDGSTATCVLAVONITLYINLMDSSRAILCRNEE 229
OY 248 SOKHAALSLSKENHPTQYFERMRIRQKAGNVRDGRVLTGLEVSRSTIGGQYKRCGCILCA 306
DB 230 SOKHAALSLSKENHPTQYFERMRIRQKAGNVRDGRVLTGLEVSRSTIGGQYKRCGCILCA 289

OY 307 PDIRRCOLTPNDRFILL-ACDGLFKVFTEPEAVNFILSCLEDEKIQREGKSADARYEA 365
DB 290 PFSRRCOLTPNDRFILLVPCDGLFKVFTEPEAVNFILSCLEDEKIQREGKSADARYEA 349
OY 366 A-CNRLANKAVORGS-ADNVTVMVVRIGH 392
DB 350 SPATRLANKAVAGARPDNVTVMVVRIGH 378
RESULT 10
ABG09336
ID ABG09336 standard; Protein; 221 AA.
XX AC ABG09336;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #9927.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB: AAS74123.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity
XX PS Claim 20; SEQ ID No 40295; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 221 AA:
Query Match 46.0%; Score 928; DB 22; Length 221;

PR	1-AUG-2000	2000S-0224516
PR	1-AUG-2000	2000S-0224513
PR	1-AUG-2000	2000S-0225211
PR	1-AUG-2000	2000S-0225214
PR	1-AUG-2000	2000S-0225266
PR	1-AUG-2000	2000S-0225677
PR	1-AUG-2000	2000S-0225568
PR	1-AUG-2000	2000S-0225570
PR	1-AUG-2000	2000S-0225547
PR	1-AUG-2000	2000S-0225157
PR	1-AUG-2000	2000S-0225758
PR	1-AUG-2000	2000S-0226759
PR	18-AUG-2000	2000S-0226579
PR	22-AUG-2000	2000S-0226681
PR	22-AUG-2000	2000S-0226682
PR	22-AUG-2000	2000S-0227182
PR	23-AUG-2000	2000S-0227019
PR	30-AUG-2000	2000S-0228924
PR	01-SEP-2000	2000S-0229827
PR	01-SEP-2000	2000S-0229343
PR	01-SEP-2000	2000S-0229443
PR	01-SEP-2000	2000S-0229545
PR	05-SEP-2000	2000S-0229595
PR	05-SEP-2000	2000S-0229613
PR	06-SEP-2000	2000S-0230436
PR	06-SEP-2000	2000S-0231442
PR	08-SEP-2000	2000S-0231443
PR	08-SEP-2000	2000S-0231144
PR	08-SEP-2000	2000S-0231143
PR	08-SEP-2000	2000S-0231414
PR	08-SEP-2000	2000S-0231080
PR	08-SEP-2000	2000S-0232081
PR	12-SEP-2000	2000S-0231968
PR	14-SEP-2000	2000S-0232197
PR	14-SEP-2000	2000S-0232198
PR	14-SEP-2000	2000S-0232299
PR	14-SEP-2000	2000S-0232400
PR	14-SEP-2000	2000S-0232401
PR	14-SEP-2000	2000S-0233063
PR	14-SEP-2000	2000S-0233064
PR	14-SEP-2000	2000S-0233655
PR	21-SEP-2000	2000S-0234223
PR	21-SEP-2000	2000S-0234274
PR	25-SEP-2000	2000S-0234997
PR	25-SEP-2000	2000S-0234998
PR	25-SEP-2000	2000S-0234999
PR	26-SEP-2000	2000S-0235684
PR	27-SEP-2000	2000S-0235684
PR	27-SEP-2000	2000S-0235636
PR	29-SEP-2000	2000S-0236576
PR	29-SEP-2000	2000S-0236567
PR	29-SEP-2000	2000S-0236568
PR	29-SEP-2000	2000S-0236569
PR	02-OCT-2000	2000S-0236602
PR	02-OCT-2000	2000S-0237037
PR	02-OCT-2000	2000S-0237038
PR	02-OCT-2000	2000S-0237039
PR	02-OCT-2000	2000S-0237040
PR	13-OCT-2000	2000S-0239935
PR	13-OCT-2000	2000S-0239937
PR	20-OCT-2000	2000S-0240960
PR	20-OCT-2000	2000S-0241221
PR	20-OCT-2000	2000S-0241785
PR	20-OCT-2000	2000S-0241786
PR	20-OCT-2000	2000S-0241877
PR	20-OCT-2000	2000S-0241808
PR	20-OCT-2000	2000S-0241826
PR	01-NOV-2000	2000S-0246414
PR	08-NOV-2000	2000S-0246417
PR	08-NOV-2000	2000S-0246475
PR	08-NOV-2000	2000S-0246476

PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246613.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0249307.
PR 17-NOV-2000; 2000US-0249308.
PR 17-NOV-2000; 2000US-0249309.
PR 17-NOV-2000; 2000US-0249310.
PR 17-NOV-2000; 2000US-0249311.
PR 17-NOV-2000; 2000US-0249312.
PR 17-NOV-2000; 2000US-0249313.
PR 17-NOV-2000; 2000US-0249314.
PR 17-NOV-2000; 2000US-0249315.
PR 17-NOV-2000; 2000US-0249316.
PR 17-NOV-2000; 2000US-0249317.
PR 17-NOV-2000; 2000US-0249318.
PR 17-NOV-2000; 2000US-0249324.
PR 17-NOV-2000; 2000US-0249325.
PR 17-NOV-2000; 2000US-0249326.
PR 17-NOV-2000; 2000US-0249327.
PR 17-NOV-2000; 2000US-0249329.
PR 17-NOV-2000; 2000US-0249399.
PR 17-NOV-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250191.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251088.
PR 05-DEC-2000; 2000US-0251179.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251890.
PR 11-DEC-2000; 2000US-0251997.
PR 05-JAN-2001; 2001us-0259678.

(HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Barash SC, Ruben SM;
PI WPI: 2001-465566/50.
XX N-PDSB; AAS41122.
DR
XX

PT Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases -
XX
PS
XX

Claim 11: SEQ ID NO 1248; 1180pp; English.

CC The present invention relates to the isolation of novel human enzyme
CC polyepitides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders, including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The

CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 138 AA:

Query Match 22.2%; Score 447.5; DB 22; Length 138;
Best Local Similarity 87.4%; Pred. No. 3,1e-35;
Matches 90; Conservative 1; Mismatches 11; Indels 1; Gaps 1;

OY 279 RDRGVLVGVLEVSRSIDGGYKKRGCVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAV 338
|||||
DB 10 RDRGVLVGVLEVSRSIDGGYKKCVTSVPDIRCOLTPNDRFILLACDGLFKVFTPEEAV 69
|||||
OY 339 NFILSCLEDEKIQTRGKSAADARVEACNRLANK-AVORGSA 380
|||||
DB 70 NFILSCLEDEKIQTRGKSAADARVEALQHAQQGCGSRGSA 112
|||||

RESULT 13
AAG18068
ID AAG18068 standard; Protein: 295 AA.
XX
AC AAG18068;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 19329.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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DT
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DE

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2

PD 06-SEP-2000.

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OY 298 YKRCGVTSVPDIRCOLTPNDRFILLACDDGLFKY 331
DB 267 FKRFGVATPDIAHAFELTERENFMILGDDGLMEV 300

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DT 06-OCT-2000 (first entry)
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DE Human secreted protein, SEQ ID NO: 7505.
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KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
PN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
PF 21-FEB-2000; 2000EP-0200610.
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PR 26-FEB-1999; 99US-0122487.
XX
PA (GEST) GENSET.
XX
PI Dumas Mline Edwards J, Duclert A, Giordano J;
XX
DR WPI: 2000-500381/45.
XX
DR N-PSDB: AAC03430.
XX
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures -

XX
PS Claim 13; SEQ ID 7505; 71bp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC regulatory sequences and to design expression and secretion vectors.
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Job time : 41 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:44:19 ; Search time 12 Seconds
(without alignments)

649,365 Million cell updates/sec

Title: US-09-935-124A-2

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	338	16.7	382	10	US-09-972-741-2
5	319	15.8	390	9	US-10-072-130-3
6	317.5	15.7	281	10	US-09-801-368-278
7	314	15.6	372	9	US-09-973-941-4
8	314	15.6	372	10	US-09-973-963-4
9	314	15.6	372	10	US-09-973-064-4
10	314	15.6	372	10	US-09-973-077-4
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12	314	15.6	372	10	US-09-973-964-4
13	314	15.6	372	10	US-09-975-072-4
14	314	15.6	372	10	US-09-972-038-4
15	314	15.6	372	10	US-09-972-457-4
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17	313	15.5	478	9	US-10-072-130-1
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19	312	15.5	400	10	US-09-925-300-1254

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23	273	13.5	371	10	US-09-828-302-15	Sequence 15, App1
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ALIGNMENTS

RESULT 1
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Sequence 2, Application US/09935124A
Patent No. US20020136003A1
GENERAL INFORMATION:
APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210US
CURRENT APPLICATION NUMBER: US/09/935, 124A
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284, 760
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-124A-2

Query Match 100.0%; Score 2018; DB 9; Length 392;
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QY 61 STATISOMVTECKGKRTSEKNSGEELVEKKCKKSSYFGKGVARERGEREE 120
Db 61 STATISOMVTECKGKRTSEKNSGEELVEKKCKKSSYFGKGVARERGEREE 120
QY 121 MODAHVILNDITECPSPSSILTRYSYFAVFGGCGTASFAAONLHQLIRKPKD 180
Db 121 MODAHVILNDITECPSPSSILTRYSYFAVFGGCGTASFAAONLHQLIRKPKD 180
QY 181 ISVEKTVKRCILDFKHTDEBFLKQASOKPARKGSRATCVLAYNDILYINLDSRAI 240
Db 181 ISVEKTVKRCILDFKHTDEBFLKQASOKPARKGSRATCVLAYNDILYINLDSRAI 240

QY	241	LCRTNEESQKAAALSLSKSEHPQTYEEMMRQKGGVNRGGRVGLGLEVSRSTGDGQYKR	300
Db	241	LCRTNEESQKAAALSLSKSEHPQTYEEMMRQKGGVNRGGRVGLGLEVSRSTGDGQYKR	300
QY	301	CGVTSVPDIRRCQLTLPNDRFLLACDGLFKVEPPEEAVNFISSLCEDEKIQTRREGKSAAD	360
Db	301	CGVTSVPDIRRCQLTLPNDRFLLACDGLFKVEPPEEAVNFISSLCEDEKIQTRREGKSAAD	360
QY	361	ARYEACNRLANKAVQRCGADNTVMVVRIGH	392
Db	361	ARYEACNRLANKAVQRCGADNTVMVVRIGH	392

```

RESULT 2
US-09-860-351-4
: Sequence 4, Application US/09860351
: Patent No. US20020077463A1
: GENERAL INFORMATION:
: APPLICANT: Millennium Pharmaceuticals, Inc.
: APPLICANT: Meyers, Rachel
: TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
: TITLE OF INVENTION: AND USES THEREFOR
: FILE REFERENCE: 38155-20013.00
: CURRENT APPLICATION NUMBER: US/09/860,351
: CURRENT FILING DATE: 2001-05-17
: PRIOR APPLICATION NUMBER: US 60/205,260
: PRIOR FILING DATE: 2000-05-19
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 4
: LENGTH: 274
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Consensus amino acid
: US-09-860-351-4

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	Query Match	19.6%	Score 395.5	DB 10	Length 274
	Best Local similarity	36.7%	Pred. No. 8.4e-28		
	Matches	106	Conservative	49	Mismatches 79
					Indels 55
					Gaps 13
QY	118 REEMODAHVILNDITRECECRPSSLLITRVSYFAVFDHGIGIRASKFAAONLQNL	--RK	174		
	118	118	118	118	118
Db	1 RKSMDAHIALKNLNLSSSSGKDSW	---SFAVFDHGIGSQAKYAGHILHITLIERKS	56		
QY	175 FPKGG-----YISVKTATYKRLDLOTFKHTDDEFLQAQS	-----QKRAMKGGSTATCVL	223		
	175	175	175	175	175
Db	57 FPEGDPMWEKMSLDLEDALKEFLE	--DTDEELBRAEKSAANKVLTKEDLSGSTATVAAL	114		
QY	224 AVDNILYLANLGDSPAILICRYNESOKHAUALSLSKHNPTQYEEMRIQKAG	---NYRD	280		
	224	224	224	224	224
Db	115 IRGNLVLVAANGDSRAVLCR--NGNAIKW-AVLTEDHKPSNDEDERERIEAGGFVSRSYN	172			
QY	281 GRVLGLVEVRSISIGGOYK-----RCG-----	-----YRSVPDI--RCQVTFN-	317		
	281	281	281	281	281
Db	173 GRVNVVLAVSARFGFELKPGSKLGPESLEANYEYISPELVYAEADPVYSTDLTFDK	232			
QY	318 DRFILLACDGLFKFTPEEAVNFILISCLEDEKIQTREGKSAADARYEAA	366			
	318	318	318	318	318
Db	233 DEFLLACDGLMDVYSDQEVDAVNSLSD-----GNKSAEDMEEA	274			

RESULT 3
 US-09-828-302-14
 : Sequence 14, Application US/09828302
 : Patent No. US20020152502A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA E SILVA, OSWALDO DA
 : APPLICANT: VAN THIELEN, NOCHA
 : APPLICANT: CHEN, ROUYING
 : APPLICANT: ISHITANI, MANABU
 : TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE

```

: TITLE OF INVENTION: IN PLANTS
: FILE REFERENCE: 16313-0029
: CURRENT APPLICATION NUMBER: US/09/828,302
: CURRENT FILING DATE: 2001-08-20
: PRIOR APPLICATION NUMBER: 60/196,001
: PRIOR FILING DATE: 2000-04-07
: NUMBER OF SEQ ID NOS: 46
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 14
: LENGTH: 353
: TYPE: PRN
: ORGANISM: Physcomitrella patens
: US-09-828-302-14

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[illegible]

Qy	376	-----	Q R G S A D N V T V M V R	389
			: : : : :	
Db	322	S P T T R Q E G C D N M S I I V Q	340	

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RESULT 4
US-09-972-741-2
Sequence 2, Application US/09972741
Patent No. US20020100070A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
TITLE OF INVENTION: MAMMESIUM-DEPENDENT PROTEIN PHOSPHATASE GENE DISRUPTIONS
FILE REFERENCE: R-723-C1P
CURRENT APPLICATION NUMBER: US/09/972,741
CURRENT FILING DATE: 2001-10-08
PRIOR APPLICATION NUMBER: US 09/815,935
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,235
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US 60/216,249
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 382
TYPE: PR1
ORGANISM: Mus musculus
US-09-972-741-2
Query Match 16.7%; Score 338; DB 10; Length 382;

```

Best Local Similarity 33.0%; Pred. No. 1,9e-22;
Matches 99; Conservative 47; Mismatches 106; Indels 48; Gaps 11;
QY 106 GLKGYAEKREEMOAHVILNDITEECPSSLTITVSVFANFQHGIRASRAAO 165
DB 21 GLRYGSSMOGRVEMEDAHVAVGL-----PSGLET-WSEFFAYIDHAGSOVAKCC 73
QY 166 NLHONLIRKFP---KGVIVSEKTVKRCLLIDTFKHTDEEFLKQASSOKPAMKDGSTATCV 222
DB 74 HLDHITNNODRGSAGAPSYE-NVKNIGITGFLIDEHMYMSKKHAGADRSTAVGV 132
QY 223 LAVDNILYIANLGDRAILLCRYNEESOKHAALSKEHNPTQYEEHMRIOKAGANVADGR 282
DB 133 LISPQHTYFINGDSRGLICR-----NRKVHFTQDHKPSNPLEKERIONAGGSVAIOR 186
QY 283 VLGLVEVSRISIDGQYKRC---CVT-----SVPIRRRCOLTLPNDRIILLACDGLPK 330
DB 187 VNGSLAVSRALCDFYK-CVHGKGPTEQLVSPPEVHDIERSE-EDDQFIILACDGIWD 243
QY 331 VTPPEAVNFILSCLE-DEKIQTRCKSAADARYAACNRLANKAVOGRSADNVYVYV 388
DB 244 VMGNELCDFVRSRLLEVTD-----LEKVCNEVYDCLYKGRSDNMAYILL 289

RESULT 5
US-10-072-130-3
Sequence 3, Application US/10072130
Patent No. US20020173022A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Golli, Surya K.
Lal, Preeti
Corley, Neil C.
Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTED for Windows Version 2.0
CURRENT APPLICATION DATA: US/10/072,130
APPLICATION NUMBER: 05-Feb-2002
FILING DATE: 05-Feb-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1247927
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-072-130-3

Query Match 15.8%; Score 319; DB 9; Length 990;
Best Local Similarity 29.4%; Pred. No. 9.0e-21;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;
QY 78 KRRTSEEEKNGSEELVEKKVCASSVIFGLKGYAEKREEMOAHVILNDITEECP 137
DB 7 KRKTEKHNAHAGN-----GLRYGSSMOGRVEMEDAHVAVGL----- 46
QY 138 PSSLTITVSVFANFQHGIRASKEPAONLHONL-----IRKPKDVI---SVKTYKR 189
DB 47 PHGL-EDWSEFFAYIDHAGSRVANCSTHLEHITTEDPRAADRSGFALEPSVE-NVKT 104
QY 190 CLDITFKHTDEEFLKQASSOKPAMKDGSPACVLAVDNIIYIANLGDRAILLCRYNEESQ 249
DB 105 GIRGFLKIDVYMNNSDLRNGMDRSGSTAVGVMSPTHITFINGDSRAVLCRNGQ--- 161
QY 250 KHAALISKEHNPTQYEEHMRIOKAGANVADGRVYGLVEVSRISIDGQYKRCG----- 302
DB 162 ---VCFSTQDHKPCNPEKERIONAGSVMIQRWGLAVSRALGDYDKVDGKGPTEQ 218
QY 303 -VTSVPIRRRCOLTLPNDRIILLACDGLFKVFTPEAVNFILSCLEDEKIQTRCKSAADA 361
DB 219 LVSPPEVYETELRAEDEFEVLACDGIWDVMSNEELCFVNSRL-----VSD 266
QY 362 RYEAACNRLANKAVOGRSADNVYVYV 388
DB 267 DLENVCNMYVDTCLHGRSDNMAYILLV 293

RESULT 6
US-09-801-368-278
Sequence 278, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Calli, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: No. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 278
LENGTH: 281
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-278

Query Match 15.7%; Score 317.5; DB 10; Length 281;
Best Local Similarity 31.4%; Pred. No. 8e-21;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;
QY 111 VAERKGE--REEMOAHVILNDITEECPSSLTITV--SVFANFQHGIRASKEPAON 166
DB 23 VAENKNSKFRMYEDVHTYVKNFA-----SRDMGYFVFGHGIGHGIDASKWCKKH 72
QY 167 LH-----ONLIRKPKGDVIVSEKTVKRCLLIDTFKHTDEEFLKQASSOKPAMKDGST-ATC 221
DB 111


```

; CURRENT APPLICATION NUMBER: US/09/973,064
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-064-4

Query Match          15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2,5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

OY 27 LFFD---LPPASSTDS-----GSGGPLLPD-----LPPASGDSG 60
|||
Db 27 LLODDRVPPTCHSSTSEPCRSRFPDGSSPATMONGIMDNRIDEPILLPSI----- 81
|||
OY 61 SLATSIQWVTEGKARKTSEEKNGSELVEKKVCASSVIFGLKGYAERKGERE 120
|||
Db 82 -----KYG-----KPIKISLENVGASQIGRRK-ENED 109
|||
OY 121 MODAHVILNDITECRPPSSLITRVSYFAVFGHGIGIRASKFAQONLHONLIRKPKGV 180
|||
Db 110 RFD---FAQLTDE-----VLTFVAYDGHGPAADCHTHMEKCIIMDLPR--- 152
|||
OY 181 ISEKTVKRCLLDTEKHTDEEFLKQA--SSQKPAWKDGSATATCYLAVDNI-LYIANIGDS 237
|||
Db 153 ---EKNLETLTLAFLIEDKAFSSHARLSADATLLTSGTATVALRDIETLVAVASGDS 209
|||
OY 238 RAILCRYNESOKHAALSISKEHNPTOYEERMRIQKAG-----NVRDGYLVLEVSR 292
|||
Db 210 RAILCR-----KGKPMKLTIDHTPERKDEKERIKKGGFVAMNSLGGPHNGRLAMTRS 263
|||
OY 293 IGDQYKRCGVTSVPDIRCOL-TPNDRFILLACDGLFVFTPEEAVNFILSCLEDEKIQ 351
|||
Db 264 IGDLDKTSVIAEPETRIKRIKLNHADSFLVLTDDGINFVMSOEICDFVNOCHDPNE-- 321
|||
OY 352 TREKSAADARYEACNRLANKAVORGSAADVVMVVRIG 391
|||
Db 322 -----AAHVTEDQAIQYTEDNSTAVVVPFG 347
|||

RESULT 10
US-09-973-077-4
; Sequence 4, Application US/09973077
; Patent No. US20020114799A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Jean-Marc
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,077
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-077-4

Query Match          15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2,5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

OY 27 LFFD---LPPASSTDS-----GSGGPLLPD-----LPPASGDSG 60
|||
Db 27 LLODDRVPPTCHSSTSEPCRSRFPDGSSPATMONGIMDNRIDEPILLPSI----- 81
|||
OY 61 SLATSIQWVTEGKARKTSEEKNGSELVEKKVCASSVIFGLKGYAERKGERE 120
|||
Db 82 -----KYG-----KPIKISLENVGASQIGRRK-ENED 109
|||
OY 121 MODAHVILNDITECRPPSSLITRVSYFAVFGHGIGIRASKFAQONLHONLIRKPKGV 180
|||
Db 110 RFD---FAQLTDE-----VLTFVAYDGHGPAADCHTHMEKCIIMDLPR--- 152
|||
OY 181 ISEKTVKRCLLDTEKHTDEEFLKQA--SSQKPAWKDGSATATCYLAVDNI-LYIANIGDS 237
|||
Db 153 ---EKNLETLTLAFLIEDKAFSSHARLSADATLLTSGTATVALRDIETLVAVASGDS 209
|||
OY 238 RAILCRYNESOKHAALSISKEHNPTOYEERMRIQKAG-----NVRDGYLVLEVSR 292
|||
Db 210 RAILCR-----KGKPMKLTIDHTPERKDEKERIKKGGFVAMNSLGGPHNGRLAMTRS 263
|||
OY 293 IGDQYKRCGVTSVPDIRCOL-TPNDRFILLACDGLFVFTPEEAVNFILSCLEDEKIQ 351
|||
Db 264 IGDLDKTSVIAEPETRIKRIKLNHADSFLVLTDDGINFVMSOEICDFVNOCHDPNE-- 321
|||
OY 352 TREKSAADARYEACNRLANKAVORGSAADVVMVVRIG 391
|||
Db 322 -----AAHVTEDQAIQYTEDNSTAVVVPFG 347
|||

RESULT 11
US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020115119A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Jean-Marc
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,063
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-063-4

Query Match          15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2,5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

OY 27 LFFD---LPPASSTDS-----GSGGPLLPD-----LPPASGDSG 60
|||
Db 27 LLODDRVPPTCHSSTSEPCRSRFPDGSSPATMONGIMDNRIDEPILLPSI----- 81
|||
OY 61 SLATSIQWVTEGKARKTSEEKNGSELVEKKVCASSVIFGLKGYAERKGERE 120
|||
Db 82 -----KYG-----KPIKISLENVGASQIGRRK-ENED 109
|||
OY 121 MODAHVILNDITECRPPSSLITRVSYFAVFGHGIGIRASKFAQONLHONLIRKPKGV 180
|||
Db 110 RFD---FAQLTDE-----VLTFVAYDGHGPAADCHTHMEKCIIMDLPR--- 152
|||
OY 181 ISEKTVKRCLLDTEKHTDEEFLKQA--SSQKPAWKDGSATATCYLAVDNI-LYIANIGDS 237
|||
Db 153 ---EKNLETLTLAFLIEDKAFSSHARLSADATLLTSGTATVALRDIETLVAVASGDS 209
|||
OY 238 RAILCRYNESOKHAALSISKEHNPTOYEERMRIQKAG-----NVRDGYLVLEVSR 292
|||
Db 210 RAILCR-----KGKPMKLTIDHTPERKDEKERIKKGGFVAMNSLGGPHNGRLAMTRS 263
|||
OY 293 IGDQYKRCGVTSVPDIRCOL-TPNDRFILLACDGLFVFTPEEAVNFILSCLEDEKIQ 351
|||
Db 264 IGDLDKTSVIAEPETRIKRIKLNHADSFLVLTDDGINFVMSOEICDFVNOCHDPNE-- 321
|||
OY 352 TREKSAADARYEACNRLANKAVORGSAADVVMVVRIG 391
|||
Db 322 -----AAHVTEDQAIQYTEDNSTAVVVPFG 347
|||
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Db 210 RAILCR-----KGRPMKLTIDHTEPERKDEKERIKKCGFVAMNSIGDPHVNGRLAMTRS 263
Oy 293 IGDGQYKRCGYTSPVDIRCOL-TPNDRFILLACDGLFVKTPPEAVNFILSCLEDEKIO 351
Db 264 IGDLDLKTSGVIAEPETKRIRKLHHAHDSFLVLTGGINFMVNSQELCPDVNCHDPNE-- 321
Oy 332 TREGKSADARYEAACNRLANKAVORGSAADVNTVAVVRIG 391
Db 332 -----AAHAVTEQAIOYGTEEDNSTAVVPEFG 347

RESULT 12
US-09-973-964-4
; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-964-4

Query Match 15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2.5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

Oy 27 LIFDD--LPPASSYDS-----GSGGPLLEDD-----LPPASSGDSG 60
Db 27 LQDDRRTVPTCHSSTSEPRCSRPDPDGSFPATWDFGIMDNRIDEPILPSSI----- 81
Oy 61 SLATSIQWVKTGEGARKRTSEEEKNGSEELVEKKVKASSVITGLGYVAERGEREE 120
Db 82 -----KYG-----KPIPKISLENVGCASQIQKRR-ENED 109
Oy 121 MODAHVILNDITEECRPPSSLITRVSYFAVFDGHCIGIRASKFAAQNLOHNLIRKPKGDV 180
Db 110 RFD-----FAQLTDE-----VLYFAVYDGHGCPAAADCFHHEKCIIMDLPK-- 152
Oy 181 ISVEKTVKRCILDTEFKHDEEFLKQA--SSQKPAWKDGSFATCVLAVDNI-LYIANLGDS 237
Db 153 ---EKNLLETLLALFLEIDKAFSSHARLSADATLLTSGTTATVALLRGIELVAVSGDS 209
Oy 238 RAILCRVNEESQKHAALSLSKEHNPTQYEEARMIOKAGS-----NVRDGRVIGLEVSVS 292
Db 210 RAILCR-----KGRPMKLTIDHTEPERKDEKERIKKCGFVAMNSIGDPHVNGRLAMTRS 263
Oy 293 IGDGQYKRCGYTSPVDIRCOL-TPNDRFILLACDGLFVKTPPEAVNFILSCLEDEKIO 351
Db 264 IGDLDLKTSGVIAEPETKRIRKLHHAHDSFLVLTGGINFMVNSQELCPDVNCHDPNE-- 321
Oy 332 TREGKSADARYEAACNRLANKAVORGSAADVNTVAVVRIG 391
Db 332 -----AAHAVTEQAIOYGTEEDNSTAVVPEFG 347

RESULT 13
US-09-975-072-4
; Sequence 4, Application US/09975072
; Patent No. US20020115607A1
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```
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/975,072
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-072-4

Query Match 15.6%; Score 314; DB 10; Length 372;
Best Local Similarity 27.5%; Pred. No. 2.5e-20;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

Oy 27 LIFDD--LPPASSYDS-----GSGGPLLEDD-----LPPASSGDSG 60
Db 27 LQDDRRTVPTCHSSTSEPRCSRPDPDGSFPATWDFGIMDNRIDEPILPSSI----- 81
Oy 61 SLATSIQWVKTGEGARKRTSEEEKNGSEELVEKKVKASSVITGLGYVAERGEREE 120
Db 82 -----KYG-----KPIPKISLENVGCASQIQKRR-ENED 109
Oy 121 MODAHVILNDITEECRPPSSLITRVSYFAVFDGHCIGIRASKFAAQNLOHNLIRKPKGDV 180
Db 110 RFD-----FAQLTDE-----VLYFAVYDGHGCPAAADCFHHEKCIIMDLPK-- 152
Oy 181 ISVEKTVKRCILDTEFKHDEEFLKQA--SSQKPAWKDGSFATCVLAVDNI-LYIANLGDS 237
Db 153 ---EKNLLETLLALFLEIDKAFSSHARLSADATLLTSGTTATVALLRGIELVAVSGDS 209
Oy 238 RAILCRVNEESQKHAALSLSKEHNPTQYEEARMIOKAGS-----NVRDGRVIGLEVSVS 292
Db 210 RAILCR-----KGRPMKLTIDHTEPERKDEKERIKKCGFVAMNSIGDPHVNGRLAMTRS 263
Oy 293 IGDGQYKRCGYTSPVDIRCOL-TPNDRFILLACDGLFVKTPPEAVNFILSCLEDEKIO 351
Db 264 IGDLDLKTSGVIAEPETKRIRKLHHAHDSFLVLTGGINFMVNSQELCPDVNCHDPNE-- 321
Oy 332 TREGKSADARYEAACNRLANKAVORGSAADVNTVAVVRIG 391
Db 332 -----AAHAVTEQAIOYGTEEDNSTAVVPEFG 347

RESULT 14
US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,038
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
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Tue Jan 21 07:12:47 2003

us-09-935-124a-2.ra1

Page

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OM protein - protein search, using sw model

Run on: January 17, 2003, 17:43:49 : Search time 17 Seconds
(without alignments)
678,458 Million cell updates/sec

Title: US-09-935-124A-2

Perfect score: 2018
Sequence: 1 MDLFGDPEPEPRRPAAGK.....KAVRGSDNVTVMVVRICH 392

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A.COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/5B.COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	100.0	392	4	US-09-013-881-2
2	340	16.8	306	3	US-08-822-701-8
3	340	16.8	306	3	US-08-325-852-8
4	326	16.2	306	4	US-08-206-646-4
5	320.5	15.9	309	2	US-08-822-701-7
6	320.5	15.9	309	3	US-08-935-853-7
7	319	15.8	390	2	US-08-873-093-3
8	319	15.8	390	4	US-08-206-646-3
9	317.5	15.7	281	2	US-08-822-701-9
10	317.5	15.7	281	3	US-08-935-855-9
11	313	15.5	478	2	US-08-873-093-1
12	313	15.5	478	4	US-08-873-093-1
13	313	15.5	479	2	US-09-206-646-1
14	271.5	13.5	314	3	US-08-822-701-10
15	271.5	13.5	314	3	US-08-935-855-10
16	269.5	13.4	392	2	US-08-822-701-2
17	269.5	13.4	392	3	US-08-935-855-2
18	269.5	13.4	542	3	US-08-935-855-20
19	255.5	12.7	546	3	US-08-935-855-20
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21	178	8.8	504	2	US-09-144-178-2
22	178	8.8	504	4	US-09-406-854-2
23	178	8.8	504	4	US-09-529-279-2
24	178	8.8	513	4	US-09-529-279-43
25	178	8.7	517	4	US-09-529-279-11
26	176	8.7	504	2	US-08-752-891-6
27	176	8.7	504	2	US-09-144-178-6

28	176	8.7	504	4	US-09-406-854-6
29	125	6.2	249	4	US-09-134-001C-4777
30	107	5.3	273	1	US-08-320-161-10
31	107	5.3	273	4	US-08-455-829-10
32	107	5.3	273	4	US-08-235-836C-13
33	107	5.3	273	4	US-08-455-873-10
34	103	5.1	475	4	US-09-370-838-193
35	100.5	5.0	466	4	US-08-235-836C-107
36	96.5	4.8	1085	2	US-08-431-080-28
37	96.5	4.8	1085	2	US-09-938-534-28
38	96.5	4.8	1085	4	US-09-845-224-28
39	95	4.7	447	4	US-09-916-109-5
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41	94.5	4.7	422	2	US-09-067-351-3
42	94.5	4.7	422	2	US-09-360-490-3
43	92.5	4.6	2756	1	US-08-375-709-11
44	92.5	4.6	2756	1	US-08-752-929-11
45	92.5	4.6	2756	4	US-09-090-793-7

ALIGNMENTS

RESULT 1
US-09-013-881-2
Sequence 2, Application US/09013881
Patent No. 6132964
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Punit
TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTA for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,881
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0470 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: KIDNNOT02
CLONE: 195647
US-09-013-881-2

Sequence 6, Appl1
Sequence 4777, Ap
Sequence 10, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 10, Appl
Sequence 193, App
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 4, Appl1
Sequence 3, Appl1
Sequence 11, Appl
Sequence 11, Appl
Sequence 7, Appl1

Query Match 100.0%; Score 2018; DB 4; Length 392;
Best Local Similarity 100.0%; Pred. No. 6.8e-201;
Matches 392; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MDLFGDLPEPPSPRPAKGEKQKPLFLFDLPPASSTDSGSGPLFDLPPASSGDSG 60
Db 1 MDLFGDLPEPPSPRPAKGEKQKPLFLFDLPPASSTDSGSGPLFDLPPASSGDSG 60
QY 61 SLATISOMVTEGKAGARKTSEEKNGSEELVEKKVCASSVIGLKGVAERGERE 120
Db 61 SLATISOMVTEGKAGARKTSEEKNGSEELVEKKVCASSVIGLKGVAERGERE 120
QY 121 MODAHVILNDITEECRPSLLTRVSYFAVEDGHGIGIRASKFAQNLHQLIRKPKGV 180
Db 121 MODAHVILNDITEECRPSLLTRVSYFAVEDGHGIGIRASKFAQNLHQLIRKPKGV 180
QY 181 ISVEVTYRCLDFTFKHDEEFLKQASSQKPAKMGSTATCYLVANDNLIYANLDSRAI 240
Db 181 ISVEVTYRCLDFTFKHDEEFLKQASSQKPAKMGSTATCYLVANDNLIYANLDSRAI 240
QY 241 LCRYNEESOKHAALSLSKEHNPTOYEERMRIOKAGNVRDGVLGVLVLEYSRISGDOYKR 300
Db 241 LCRYNEESOKHAALSLSKEHNPTOYEERMRIOKAGNVRDGVLGVLVLEYSRISGDOYKR 300
QY 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVTPPEAVNFILSCLDEKIQTRKGSAD 360
Db 301 CGVTSVPDIRRCQLTPNDRFILLACDGLFKVTPPEAVNFILSCLDEKIQTRKGSAD 360
QY 361 ARYEACNRANKAVORGADNVTVMVVRIGH 392
Db 361 ARYEACNRANKAVORGADNVTVMVVRIGH 392
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RESULT 2

US-08-822-701-8
Sequence 8, Application US/08822701
Patent No. 5976853

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
APPLICANT: Basillio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Rattus

Query Match 16.8%; Score 340; DB 2; Length 306;
Best Local Similarity 33.7%; Pred. No. 6e-27;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

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QY 106 GIKGYAERKGEREMODAHVILNDITEECRPSLLTRVSYFAVEDGHGIRASKFAAQ 165
Db 21 GLRYGLSMQGWRYEMEDAHVILNDITEECRPSLLTRVSYFAVEDGHGIRASKFAAQ 165
QY 166 NLHQLIRKFP-KCD-VISVEYTKRCLDFTFKHDEEFLKQASSQKPAKMGSTATCY 222
Db 74 HLHDITNNODFKSGAGASVE-NVKNIGIRGFLBIDHMRVMSKKHGAIRSGSTAVGV 132
QY 223 LAVDNILYIANLGDRLALCRYNEESOKHAALSLSKEHNPTOYEERMRIOKAGNVRDGR 282
Db 133 LISPHITTFINCGDSRGLCR-----NRKYHFTQDKRPSNPLEKXRIQNNAGSVMIOR 186
QY 283 VLGVLVSRISGDOYKRC---GVT-----SVPDIRRCQLTPNDRFILLACDGLFK 330
Db 187 VNGSLAVSRALGDFDYK-CVHGKQPTQLVSPREVDHIERSE--EDDQFIILACDGIWD 243
QY 331 VTPPEAVNFILSCLDEKIQTRKGSADARIEACNRANKAVORGADNVTVMV 388
Db 244 VMGNEILCDFVRSRLVETD-----DEKVCNEVDYCLYKGRDNMSVILI 289
```

RESULT 3

US-08-935-855-8
Sequence 8, Application US/08935855
Patent No. 6066485

GENERAL INFORMATION:

APPLICANT: Guthridge, Mark
APPLICANT: Basillio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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Page 3

MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Rattus
US-08-935-855-8

Query Match 16.8%; Score 340; DB 3; Length 306;
Best Local Similarity 33.7%; Pred. No. 6e-27;
Matches 101; Conservative 47; Mismatches 104; Indels 48; Gaps 12;

QY 106 GLGYAERKGEREMODAHVILNDITEECRPPSLITRVSYFAVFDGHSRASKFAAQ 165
DB 21 GLRYGLSSMOGWRVEMEDAHVAVIGL-----PSGLER-WSEFVAYDGHAGSSVARYCE 73
QY 166 NLQNLRKRP-KGD--VISVEKTVKRCLLDPFKHTDEEFLLKQASSQKPAWKDGSTATCV 222
DB 74 HLDHITNNODERKSGAGASVE-NVKNIGITGLETIDEMRVSEKHHGADRSSTAVGV 132
QY 223 LAVDNILYIANLGDSTRATLCRYNEESQKHAALSLSKEHNPQYEEKRIQAGVPRDGR 282
DB 133 LISPOHTYFINGDSRGLCLR-----NRKVFETQDHPSPLEKEKTIQAGSVAIQK 186
QY 283 VLGVLEYSRISDGOYKRC---GVT-----SVDIRCQLTPNDRFTLLACGLER 330
DB 187 VNGSLAVSRALDQDFDK-CVHGKPGTQOLVSPEPEVHDEKSE--EDQFILLACDQIMD 243
QY 331 VFTPEAVNFIISCLE--DEKIQREKSAADARYACNRLANKAVORGADNVYMYV 388
DB 244 VMGNEELCDEVRSLRELVTD-----LEKVCNEVVDICLYKSGRDMNSVILI 289

RESULT 4
US-09-206-646-4
Sequence 4, Application US/09206646
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil G.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319.1.D1
CURRENT APPLICATION NUMBER: US/09/206,646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ. ID NOS: 4
SOFTWARE: PERL Program
SEQ. ID NO: 4
LENGTH: 390
TOPOLGY: linear
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: ID No. 6436637 9452526
US-09-206-646-4

Query Match 15.2%; Score 326; DB 4; Length 390;
Best Local Similarity 30.0%; Pred. No. 2.5e-25;
Matches 98; Conservative 52; Mismatches 121; Indels 56; Gaps 10;
QY 78 KRKTSSEKNGSEELVKKVCKASSVIFGLKGYAERKGEREMODAHVILNDITEECRP 137
DB 7 KRTEKHNAHAGN-----GLRYGLSSMOGWRVEMEDAHVAVIGI-----46
QY 138 PSSLITRVSYFAVFDGHSRASKFAAONLHONL-----IRKFPK-GDVI--SVKTVKR 189
DB 47 PHGL-DNMSFFAVYDGHAGSRVANYCSTHLEHITTTNEDFRADKSGSALSPSVK 104
QY 190 CLDGFKHTDEEFLLKQASSQKPAWKDGSTATCVLAVDNILYIANLGDSTRATLCRYNEESQ 249
DB 105 GRTGFLKIDEMYMNFSDLRNGMDRSGTAVGVAVVSPTHMYFINGDSRAVLCRNGQ---161

QY 250 KHAALSKEHNPQYEEKRIQAGVPRDGRVLGVLEYSRISDGOYKRC-----302
DB 162 ---VCFSTQDHRKPCNPVEKERTIQAGSVAIQKNSLAVSRALDQIDYCVGKPGTQ 218
QY 303 -VTSVDIRCQLTPNDRFTLLACDGLFKYFTPEAVNFIISCLEDEKIQREGKSAADA 361
DB 219 LVSPPEVEIYRAEDEFEVYVACDGIWDMSEBELCEFYKSRLE-----VSD 266
QY 362 RYEPACNRLANKAVORGADNVYMYV 388
DB 267 DLNVCNMYVDICLYKSGRDMNSVILI 289

RESULT 5
US-08-822-701-7
Sequence 7, Application US/08822701
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SPOUNCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Mus musculus
US-08-822-701-7

Query Match 15.9%; Score 320.5; DB 2; Length 309;
Best Local Similarity 29.7%; Pred. No. 6.5e-25;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;
QY 78 KRKTSSEKNGSEELVKKVCKASSVIFGLKGYAERKGEREMODAHVILNDITEECRP 137
DB 7 KRTEKHNAHAGN-----GLRYGLSSMOGWRVEMEDAHVAVIGI-----46
QY 138 PSSLITRVSYFAVFDGHSRASKFAAONLHONL-----IRKFPK-GDVI--KTV 187
DB 47 PHGL-DNMSFFAVYDGHAGSRVANYCSTHLEHITTTNEDFRADKSGSALSPSVK 105
QY 188 KRCLDTEKHDEEFLLKQASSQKPAW-KDGSTATCVLAVDNILYIANLGDSTRATLCRYNE 246

Db 106 RTGFLKI-----DEYMRNFSDLRNGDRSGSTAVGVWVSPTHMFTINCDSRAVLCRNQ 160
Qy 247 ESQKHAALSLSKHNPTQYEEBMRIOKAGNVRDGVLCGLEVSRSIGDQYKRCG----- 302
Db 161 -----VCSFTGDHRCNPKVEKERIONAGSVMIQIRVNSLAVSRALDGYDKCVDKGP 214
Qy 303 ----VTSVPDIRRCQLTENDRIFLLACDGLFVFTPEEAVNFILSCLEDEKIQTREGKSA 358
Db 215 TEOLVSPPEVEYEIVRAEDEFVVLACDGIWVMSNEELCEFEVKSRL----- 262
Qy 359 ADARYEACNRLANKAVORGSAADNTVMVY 388
Db 263 VSDLEENVCNMYVDTCLHKGRSDNMSVLY 292

RESULT 6
US-08-935-855-7
Sequence 7, Application US/08935855
Patent No. 6066485

GENERAL INFORMATION:
APPLICANT: Gulbridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Mus musculus

US-08-935-855-7

Query Match 15.9%: Score 320.5; DB 3; Length 309;
Best Local Similarity 29.7%; Pred. No. 6.5e-25;
Matches 98; Conservative 54; Mismatches 115; Indels 63; Gaps 12;

Qy 78 KRKTSEERKNGSEELVERKVKCASSVIFGLKGYAERKGEREMODAHVILNDITEECRP 137
Db 4 KRKTSEERKNGSEELVERKVKCASSVIFGLKGYAERKGEREMODAHVILNDITEECRP 137
Qy 138 PSSLTRSYFAVDPDGHGICIRASKRAAONLHONL-----IRKFPK-GDVI--SVE--KTV 187
Db 4 PSSLTRSYFAVDPDGHGICIRASKRAAONLHONL-----IRKFPK-GDVI--SVE--KTV 187

Db 47 PHGL-DNMSFFAVDYGAGSRVANYCSTHLEHTTNEDEFRADKSGSALEPSVESVYTG 105
Qy 188 KRCLDTEFKHTDEEFLKQASSOKPAM-KDGSATATCVLAVNDLIYIANLGDSPAILCRVNE 246
Db 106 RTGFLKI-----DEYMRNFSDLRNGDRSGSTAVGVWVSPTHMFTINCDSRAVLCRNQ 160
Qy 247 ESQKHAALSLSKHNPTQYEEBMRIOKAGNVRDGVLCGLEVSRSIGDQYKRCG----- 302
Db 161 -----VCSFTGDHRCNPKVEKERIONAGSVMIQIRVNSLAVSRALDGYDKCVDKGP 214
Qy 303 ----VTSVPDIRRCQLTENDRIFLLACDGLFVFTPEEAVNFILSCLEDEKIQTREGKSA 358
Db 215 TEOLVSPPEVEYEIVRAEDEFVVLACDGIWVMSNEELCEFEVKSRL----- 262
Qy 359 ADARYEACNRLANKAVORGSAADNTVMVY 388
Db 263 VSDLEENVCNMYVDTCLHKGRSDNMSVLY 292

RESULT 7
US-08-873-093-3
Sequence 3, Application US/08873093
Patent No. 5853997

GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1247927
US-08-873-093-3

Query Match 15.8%: Score 319; DB 2; Length 390;
Best Local Similarity 29.4%; Pred. No. 1.3e-24;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;
Qy 78 KRKTSEERKNGSEELVERKVKCASSVIFGLKGYAERKGEREMODAHVILNDITEECRP 137
Db 4 KRKTSEERKNGSEELVERKVKCASSVIFGLKGYAERKGEREMODAHVILNDITEECRP 137

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us-09-935-124a-2.ra1

Page 5

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Db      7 KRKTEKHNHAGAGN-----GLRYGLSSMOGRMEVEDAHHTAVVGI-----46
Oy      138 PSSLTITRVSYFAVFDGCGIRASKFAAONLHONT-----IRKPKGDVT---SVKTYKR 189
Db      47 PIGL-EDMSFFAVYDGHAGSRVANYSHTLHEHTTNEDEFAADKSGFALPESVE-NVKT 104
Oy      190 CLIDPEFKHTDEEFLKQASSOKPAMKDGSTATCVLAVNDIILYIANLGDRAILCRNESQ 249
Db      105 GIRTGFLKIDEMRNFSDLNRNGMDRSGTAAGVMTSPHTIYFINGDSRAVLGRNQ-----161
Oy      250 KHAALSLSKENHPTQYEBERRKIQACGNVDRGVLGVLEVSRTIGDQYKRG-----302
Db      162 ---VCFSTQDHRPCNPMKEKEKIONAGSGVMIDRVNGSLAVSRALGDYDKCYDQKGPTEQ 218
Oy      303 -VTSVPDIRCOLTPNDFILLACDGLFVFTPEEAVNFILSCLEDEKIQTRGKSADA 361
Db      219 LVSPEVEYELLRAEEDFEVVLACDDGIMVMSNEELCEFNARLE-----VSD 266
Oy      362 RYEACNRLANKAVORGSAADNVTVVY 388
Db      267 DLENVCNMYVDTCILHKSGRDMSTIVL 293

RESULT 8
US-09-206-646-3
Sequence 3, Application US/09206646
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319-1 DIV
CURRENT APPLICATION NUMBER: US/09/206,646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 3
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: ID No. 6436637 g247927
US-09-206-646-3

Query Match      15.8%: Score 319; DB 4; Length 390;
Best Local Similarity 29.4%: Pred. No. 1.3e-24;
Matches 96; Conservative 51; Mismatches 124; Indels 56; Gaps 9;

Db      7 KRKTEKHNHAGAGN-----GLRYGLSSMOGRMEVEDAHHTAVVGI-----46
Oy      138 PSSLTITRVSYFAVFDGCGIRASKFAAONLHONT-----IRKPKGDVT---SVKTYKR 189
Db      47 PIGL-EDMSFFAVYDGHAGSRVANYSHTLHEHTTNEDEFAADKSGFALPESVE-NVKT 104
Oy      190 CLIDPEFKHTDEEFLKQASSOKPAMKDGSTATCVLAVNDIILYIANLGDRAILCRNESQ 249
Db      105 GIRTGFLKIDEMRNFSDLNRNGMDRSGTAAGVMTSPHTIYFINGDSRAVLGRNQ-----161
Oy      250 KHAALSLSKENHPTQYEBERRKIQACGNVDRGVLGVLEVSRTIGDQYKRG-----302
Db      162 ---VCFSTQDHRPCNPMKEKEKIONAGSGVMIDRVNGSLAVSRALGDYDKCYDQKGPTEQ 218
Oy      303 -VTSVPDIRCOLTPNDFILLACDGLFVFTPEEAVNFILSCLEDEKIQTRGKSADA 361
Db      219 LVSPEVEYELLRAEEDFEVVLACDDGIMVMSNEELCEFNARLE-----VSD 266
Oy      362 RYEACNRLANKAVORGSAADNVTVVY 388
```

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Db      267 DLENVCNMYVDTCILHKSGRDMSTIVL 293

RESULT 9
US-08-822-701-9
Sequence 9, Application US/08822701
Patent No. 5976483
GENERAL INFORMATION:
APPLICANT: Guthridge, Mark
APPLICANT: Basilio, Claudio
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US-08-822-701-9

Query Match      15.7%: Score 317.5; DB 2; Length 281;
Best Local Similarity 31.4%: Pred. No. 1.1e-24;
Matches 95; Conservative 44; Mismatches 93; Indels 71; Gaps 12;

Oy      111 VAEKRG--REEMODAHVILNDITEBCRPSSLITRV--SYFAVFDGCGIRASKFAAON 166
Db      23 VAENKNSKFRKTMEDVITVKNFA-----SRIDMGYIAVFDGCHGIDASWCKKH 72
Oy      167 LH-----ONLIRKPKGDVISEVETKYKRCILDITFKHTDEEFLKQASSOKPAMKDGST-ATC 221
Db      73 LHFTIIEONL-----ADETDVADYLDNSFLAIDET-----NFKLVGSGCTAAVC 119
Oy      222 VL---AVNT-----LYTANGOSRAILCRYNESQKHAALSLSKENHPTQY 265
Db      120 VLWELIPDSVSDSDMDLAQHORLITYANAGDSRIYLFENGK-----STRUTYDKHASDT 173
Oy      266 EERRKIQACGNVDRGVLGVLEVSRTIGDQYKRGCVTSVPOIRCOLTPNDFILLAC 325
Db      174 LEMORQAGGGLIKSRVNGMLAVTRSLQDKFDSLVVGS-PFTTSVEITSDEKFLIILAC 232
Oy      326 DGLFKYFTPEEAVNFILSCLEDEKIQTRGKSADARVEACNRLANKAVORGSAADNVTV 385
```


QY 250 KHAALSLSKEHNPQYEEERMRIOKAGNVPRDGVLYGLEVSRISIGDGYKRCG----- 302
DB 162 ---VCFSTQDHRKPCNPREKERIONAGGSVMIORVNGSLAVSRALGDDYDKCYDGGKPTQ 218
QY 303 -VTSVPDIRRCQLPNDPFIILACDGLFKVFTPEEAVNFILISCLDEKIQTRGKSADA 361
DB 219 LVSPEPEVEYELIRAEDEFFIILACDGIWDMVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEACNRLANKAVQSGADNVTVMYV 388
DB 267 DLENVCNMVVDTCILHKGRDMSIIV 293

RESULT 12

US-08-873-093-4
Sequence 4, Application US/0873093
Patent No. 5853997
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/873,093
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1452526

US-08-873-093-4

Query Match 15.5%; Score 313; DB 2; Length 478;
Best Local Similarity 28.7%; Pred. No. 7,8e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;
QY 78 KKRTSEEEKNGSEELVEKKYKCRASSVIFGLKGYAEKRGREEMODAHYILNDITEECRP 137
DB 7 KKRTSEEHNAAGN-----GLRYGLSSMOGRVEMEDAHAAVVG----- 46
QY 138 PSSLTIRVSYFAVPDGHGIRASKFAQNLHONLIR-----KPKGDVTSVEKTVKR 189
DB 47 PHGL-EDWSFPAVVDGHAGSRVANCSTHLEHTTTNEDFPAAGKSGSALSLELSE- NVKN 104

QY 190 CLIDTFKHTDEFLKQASSOKPAMKDGSTATCVLAVDNILYIANLGRRAILCRYNESQ 249
DB 105 GIRTGFLKIDEXMKNFSDLRNGMDRSGTAVGVMISPRHIIFFINCGBSRVILYRNGQ--- 161
QY 250 KHAALSLSKEHNPQYEEERMRIOKAGNVPRDGVLYGLEVSRISIGDGYKRCG----- 302
DB 162 ---VCFSTQDHRKPCNPREKERIONAGGSVMIORVNGSLAVSRALGDDYDKCYDGGKPTQ 218
QY 303 -VTSVPDIRRCQLPNDPFIILACDGLFKVFTPEEAVNFILISCLDEKIQTRGKSADA 361
DB 219 LVSPEPEVEYELIRAEDEFFIILACDGIWDMVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEACNRLANKAVQSGADNVTVMYV 388
DB 267 DLENVCNMVVDTCILHKGRDMSIIV 293

RESULT 13

US-09-206-646-1
Sequence 1, Application US/09206646
Patent No. 6436637
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Lal, Preeti G.
APPLICANT: Corley, Neil C.
APPLICANT: Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
FILE REFERENCE: PF-0319-1-DIV
CURRENT APPLICATION NUMBER: US/09/206,646
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 479
TYPE: PRP
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID NO. 6436637 013177CD1
US-09-206-646-1

Query Match 15.5%; Score 313; DB 4; Length 479;
Best Local Similarity 28.7%; Pred. No. 7,9e-24;
Matches 94; Conservative 52; Mismatches 125; Indels 56; Gaps 8;
QY 78 KKRTSEEEKNGSEELVEKKYKCRASSVIFGLKGYAEKRGREEMODAHYILNDITEECRP 137
DB 7 KKRTSEEHNAAGN-----GLRYGLSSMOGRVEMEDAHAAVVG----- 46
QY 138 PSSLTIRVSYFAVPDGHGIRASKFAQNLHONLIR-----KPKGDVTSVEKTVKR 189
DB 47 PHGL-EDWSFPAVVDGHAGSRVANCSTHLEHTTTNEDFPAAGKSGSALSLELSE- NVKN 104
QY 190 CLIDTFKHTDEFLKQASSOKPAMKDGSTATCVLAVDNILYIANLGRRAILCRYNESQ 249
DB 105 GIRTGFLKIDEXMKNFSDLRNGMDRSGTAVGVMISPRHIIFFINCGBSRVILYRNGQ--- 161
QY 250 KHAALSLSKEHNPQYEEERMRIOKAGNVPRDGVLYGLEVSRISIGDGYKRCG----- 302
DB 162 ---VCFSTQDHRKPCNPREKERIONAGGSVMIORVNGSLAVSRALGDDYDKCYDGGKPTQ 218
QY 303 -VTSVPDIRRCQLPNDPFIILACDGLFKVFTPEEAVNFILISCLDEKIQTRGKSADA 361
DB 219 LVSPEPEVEYELIRAEDEFFIILACDGIWDMVMSNEELCEYKSRLE-----VSD 266
QY 362 RYEACNRLANKAVQSGADNVTVMYV 388
DB 267 DLENVCNMVVDTCILHKGRDMSIIV 293

RESULT 14

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US-08-822-701-10
; Sequence 10, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: FLOOR
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-943-1684
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Leishmania
; US-08-822-701-10

Query Match 13.5%; Score 271.5; DB 2; Length 314;
Best Local Similarity 28.0%; Pred. No. 8e-20; Indels 83; Gaps 12.
Matches 84; Conservative 43; Mismatches 90;

OY 116 GEREMODAHVTLNDITECRPPSLITFVSYFAVFDGCHGRASKFAONLHONLRKF 175
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 31 GYRETMEDAHL-----TYLTDWGFGFYFDGHVNDQCSOYLERRARS----- 72

OY 176 PKGDIVSEYKTVKRLDLOTFKHPTDEEFLKQASSQRPAMKD-----GSTATCYLAVDN--- 227
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 73 -----ALEK-----ESIPMTDERMKELALRIDQEWMDSGREGSGTFFVALKEGKK 119

OY 228 -ILYIANYLGDSTAILLCRYNEESQKNAALSLSKEHNPTQYEEEMRKIOKAGNVRDGRVLCV 286
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 120 VHLQGVNGVYKDSRVVAC-----IDGVCVPLTIDHKKPNNEGEQRILENCGRVRENNNDVDS 173

OY 287 LEVRSISIGDGYK-----RCGYTSVPIIRRCOLT--PNDRFILLACDGLRK-VTPPE 336
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 174 LAVSAFAFDREKRLKSGSLQLEQKVTALADVQKDTFFDSND--FVLLCCGVFEQGNFPNEE 232

OY 337 AVNFIICLEDKIOTRECKSAADARYEACN-----RLANKAVORGSADNVTVMYVR 389
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 233 VYAVYKQOLE-----TCNDLAEVAGRVCEAEIERSRDNISCHIVQ 273

RESULT 15
US-08-935-855-40

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: Sequence 1 Application US/08935855
: Patent No. 6066485
:
: GENERAL INFORMATION:
: APPLICANT: Guthridge, Mark
: APPLICANT: Basilio, Claudio
: TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
: TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
: NUMBER OF SEQUENCES: 22
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: David A. Jackson, Esq.
: STREET: 411 Hacksack Ave, Continental Plaza, 4th
: STREET: Floor
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/935,855
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Jackson Esq., David A.
: REGISTRATION NUMBER: 26,742
: REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-487-5800
: TELEFAX: 201-343-1684
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 314 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: ORGANISM: Leishmania
:
: US-08-935-855-10
:
: Query Match 13.5%, Score 271.5; DB 3; Length 314;
: Best Local Similarity 28.0%; Pred. No. 8e-20;
: Matches 84; Conservative 43; Mismatches 90; Indels 83; Gaps 12;
:
: Oy 116 GEREMOAHYIANDITECRPPSLITRVSGFAVFDGCGIRASKFAAQNHLQNLKIF 175
: | | | | | : | | | | | : | | | | | : | | | | | :
: Db 31 GIRETMEAHNL-----TILTDSWGFVGVGDGVANDQCSQYLERAMRS----- 72
:
: Oy 176 PKGDIVSEKTVKRCILDTFKHTDEEFLKQASSQKPAWKD-----GSTATCVLAVDN--- 227
: | | | | | : | | | | | : | | | | | : | | | | | :
: Db 73 -----ALEK-----BSIPWTERMKELRLRIDQEMDMSGREGSGCTGFVALKEGKN 119
:
: Oy 228 -ILYIANTGDSFAILICRNYESQKHAALSLEKHNPTQYEERMRIOKAGVNRGCRVLGV 286
: | | | | | : | | | | | : | | | | | : | | | | | :
: Db 120 VHLGANGNDSRVAC-----IDGVCVPLTEDHKPNNEGERORLENCAGRVENNRVDGS 173
:
: Oy 287 LEVSGSIDDGOK-----RCGYVSVPIIDIRCOLT---PNDRFILLACDGLFK-VFPDEE 336
: | | | | | : | | | | | : | | | | | : | | | | | :
: Db 174 LAVSAFEDPREKLAGSGGLEOKYATLADVQKHDPFTDPSND-FVLLCCDGVFEGNFPEE 232
:
: Oy 337 AVNFIISLCEDEKTIOTREGKSAADARYEACN-----RLANKAVQGSADNVTVMVVR 389
: | | | | | : | | | | | : | | | | | : | | | | | :
: Db 233 VVAVYVKKOLE-----TCNDLAEVAGRVCEAIRIEGRSDRNISCMITVQ 273

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